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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM nucleic - nucleic search, using sw model
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July 30, 2005, 10:32:26; Search time 308.446 Seconds (without alignments) 479.804 Million cell updates/sec

US-09-544-776-3 25 Title:

Perfect score:

1 cuggauagcuuggaucacacccuug 25 Sequence:

IDENTITY_NUC Scoring table: 4390206 seqs, 2959870667 residues Searched:

Gapop 10.0 , Gapext 1.0

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

N_Geneseq_16Dec04:* geneseqn1990s:* geneseqn1980s:* Database

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2001as:* geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

SUMMARIES

AAV3697 Human NSP AA441193 Human NGC AA590323 Human NGG Abn96987 Gene #348 Ab189601 Human pol Aa47283 Human NSP Aav23695 Human NSP Aax37587 Extended Adp18854 Human sec Acc81058 Human Nog Acc81059 Human Nog Acc81054 Human Nog Acc81055 Human Nog Acc81056 Human Nog Adc16424 Nucleotid Adr13967 Human Nog Acc81049 Human Nog Acc81049 Human Nog Acc81057 Human Nog Description ACC81055 ACC81056 ADQ16424 ADR13967 ACC81049 ACC81057 ACC81058 ACC81059 ACC81054 AAX41193 AAF90323 ABN96987 AAA72983 AAV23695 ABL89601 AAC64407 AAV23697 DB Query Match Length 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 Score Result Š.

Aaf90325 Human NOG	Aax04379 Human sec	Aba05903 Human RTN	Abk34580 Human cDN	Adi62860 Human apo	Aaz36230 cDNA enco	Aad08386 Human sec	Aak94408 Human ful	Adl31137 Full leng	Aaf32725 Human sec	Adk14166 Human aut	Abk90135 DNA encod	Aai98079 Human neu	Abk90133 DNA encod	Abv94681 Human pan	Aac64406 Human Nog	Aav30920 Human sec	Aaf98399 Human cDN	Adi31056 Human cDN	Adq16433 Construct	Aazs6886 Human MAG	Aaf90324 Human NOG	Abk90134 DNA encod	Abn86601 Human neu	Ado07886 Human pol
AAF90325	AAX04379	ABA05903	ABK34580	AD162860	AAZ36230	AAD08386	AAK94408	ADL31137	AAF32725	ADK14166	ABK90135	AAI98079	ABK90133	ABV94681	AAC64406	AAV30920	AAF98399	ADI31056	ADQ16433	AAZ56886	AAF90324	ABK90134	ABN86601	AD007886
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
25	25	22	25	22	22	25	25	25	25	25	25	52	25	25	25	25	22	52	22	22	22	25	25	22
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ALIGNMENTS

RESULT 1

Human, Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; antisense; Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:3. /*tag= a /note= "phosphorothioate linkages" Location/Qualifiers BP. AAC64407 standard; RNA; 25 (first entry) phosphorothioate; ss. Key modified_base 08-FEB-2001 Homo sapiens AAC64407; AAC64407

WO200060083-A1

12-OCT-2000

07-APR-2000; 2000WO-US009383

99US-0128372P. 99US-0140331P. 38-APR-1999; 21-JUN-1999;

(CHIR) CHIRON CORP.

Williams LT; Wei D, Halenbeck R,

WPI; 2000-665007/64.

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

Aaz56888 Human MAG

AAX97587 ADP18854 AAZ56888

%X000000000000000X

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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl. human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of Pl with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The MgR polyapetide or an agent inhibits the binding of Nogo to NgR of Olypeptide or an agent inhibits the binding of Nogo to NgR of Olypeptide or an agent inhibits the binding of Nogo to NgR of Olypeptide or an agent inhibits the binding of Nogo to NgR or NgR poinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalopathy, panencephalopathy, panencephalopathis, or Krabbe's disease. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75 BP; 25 A; 15 C; 18 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.06
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CUGGAUAGCUUGGAUCACACCCUUG 25
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CTGGATAGCTTGGATCACCCCTTG 12
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tes 18; Conservative
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/product=
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                                    The present invention describes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polymocleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CNS; Nogo; spinal cord injury; carnial trauma; serioke; Krabbe's disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
                                                                                                                                                                                                                                                                                        polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligonucleotide from the present invention
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/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Nogo receptor inhibitor Pepl cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CUGGAUAGCUUGGAUCACACCCUUG
Claim 25; Page 32; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2001; 2001US-00972599.
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Les 25; Conservative
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Gaps

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DB 9; Length 75; 0; Indels

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Human, Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CMS; Nogo; spinal cord injury; cranial trauma; spinal trauma; stroke; Krabbe's disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system
                                                                                                                                                                                                                                                                   /note= "No start/stop codon given"
                                                                                                                                                                                                                                                       "Partial human NogoA"
                                                                                                                                                                                                                  Location/Qualifiers
ACC81057 standard; cDNA; 75 BP.
                                                                                                                                                                                                                                                                                                                                              34-OCT-2002; 2002WO-US032007.
                                                                                                                                                                                                                                                                                                                                                                       06-OCT-2001; 2001US-00972599
                                                                         Human NogoA partial gene #2.
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Disclosure, Page 135; 148pp; English

us-09-544-776-3.rng

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                                                         The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl, human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of Pl with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no main, provided that a partial CTS domain, if present, consists of no more than the first 13 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polymucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR polypeptide or an agent inhibite the binding of Nogo to NgR or NgR polypeptide or an agent inhibite the binding of Nogo to NgR or NgR polyal in treating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal cord injury, encephalopathy, panencephalitis, or Krabbe's disease. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CNS; Nogo; spinal cord injury; cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
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central nervous system disease, disorder or
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CTGGATAGCTTGGATCACACCCTTG 9
                                     Disclosure; Page 139; 148pp; English
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neuron, or in treating central n
injury, e.g. spinal cord injury.
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ACC81058/c
ID ACC81058 standard; cDNA; 90
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/product=
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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl, human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of Pl with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no convertion has neuroprotective acidity. The polynucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NGR polypeptide or an agent inhibite the binding of Nogo to NGR or NGR dependent signal transduction in the central nervous system neuron may be used in treating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NGR protein may be associated with thibition of axonal responsability and provided or an injury, e.g. inhibition of axonal responsability or injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
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New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or injury, e.g. spinal cord injury.
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sequence is used in the exemplification of the invention
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ive 7; Mismatches
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                                                                                                                                                                                              Disclosure, Page 140; 148pp; English.
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Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; axonal growth; central nervous system; CMS; Nogo; spinal cord injury; cranial trauma; spinal trauma; stroke; Krabbe; disease; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human Nogo receptor inhibitor Pep2-41"
/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Nogo receptor inhibitor Pep2-41 cDNA.
                                                                                                       Disclosure; Page 140; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                   1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             33 CTGGATAGCTTGGATCACACCCTTG
                                                                                    injury, e.g. spinal cord injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC81054 standard; cDNA; 120 BP
                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 72.0%;
es 18; Conservative 7
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                           WPI; 2003-393433/37.
                                      P-PSDB; ABR59678
         Strittmatter SM;
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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl, human Nogo receptor (NgR) NTRRCT domain), or residues 27-309 of Pl with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polynucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR polypeptide or an agent inhibite the binding of Nogo to NgR or NgR-capedient signal transduction in the central nervous system neuron may be used in treating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, cerebral or spinal trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophalatic demyelination, encephalomyelitis, multifocal material mat
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                                                                                                                                                                                                                                                                                                                                                                  New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or injury, e.g. spinal cord injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 137; 148pp; English.
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                                   06-OCT-2001; 2001US-00972599.
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Best Local Similarity 72.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                             WPI; 2003-393433/37
                                                                                                         (UYYA ) UNIV YALE
                                                                                                                                                                                       Strittmatter SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (PI, human Nogo receptor (NgR) WITART domain), or residues 27-309 of PI with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polymucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR capendent signal transduction in the central nervous system neuron may be cused in treating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with containing cancer and demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalogathy, panencephalitis, or Krabbe's disease. The present
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                                                                                                                                                                                                                  New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or
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Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy; cannal growth; central nervous system; CNS; Nogo; spinal cord injury; cranial trauma; spinal trauma; stroke; Krabbe's disease; campialinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene; Human Nogo receptor binding region DNA. Location/Qualifiers 1. .198 Homo sapiens 8X11111X8X44444X6X6X6XXXXX

(first entry)

22-JUL-2003

ACC81055;

WO2003031462-A2

/*tag= a /product= "Human Nogo receptor binding region" /note= "No start/stop codon given"

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The invention relates to a novel nucleic acid encoding a polypeptide comprising amino acid residues 27-309 of a 473 amino acid sequence (PI, human Mogo receptor (MR) NTLERCT domain), or residues 27-309 of PI with 1-20 conservative amino acid substitutions, and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive residues. The nucleic acid of the invention has neuroprotective activity. The polynucleotide may have a use in gene therapy. The nucleic acid is useful for decreasing inhibition of axonal growth by a central nervous system (CNS) neuron. The NgR polypeptide or an agent inhibits the binding of Nogo to NgR or NgR copypeptide or an agent inhibits the binding of Nogo to NgR or NgR copypendent signal transduction in the central nervous system neuron may be used in treating central nervous system disease, disorder or injury, e.g. spinal cord injury. Expression of an NgR protein may be associated with inhibition of axonal regeneration following cranial, carebral or spinal trauma, stroke or a demyelinating disease, such as multiple sclerosis, purposite demyelinating disease, such as multiple sclerosis, purpositive demonphasic demyelination, encephalomyelitis, multifocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human Nogo receptor polypeptides and nucleic acids, useful for decreasing inhibition of axonal growth by a central nervous system neuron, or in treating central nervous system disease, disorder or
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/product= "Partial human NogoA"
/note= "No start/stop codon given"
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Best Local Similarity 72.0%; Pred. No. 0.07;
Matches 18; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 139; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 CTGGATAGCTTGGATCACACCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trauma, stroke or a demyelinating disease, such as multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, or Krabbe's disease. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 25; DB 9; Length 198;
Pred. No. 0.079;
7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 198 BP; 54 A; 36 C; 48 G; 60 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury, e.g. spinal cord injury.
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illarity 72.0%; 1
Conservative 7
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                                                                               34-OCT-2002; 2002WO-US032007
                                                                                                                                  36-OCT-2001; 2001US-00972599
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P-PSDB; ABR59674.
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les 18; Conserv
                                                                                                                                                                                     (UYYA ) UNIV YALE
                                                                                                                                                                                                                                           Strittmatter SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                         17-APR-2003
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Gaps

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ACC81056/c

RESULT

Best Loca Matches

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derivative comprising a mutation in or flanking MAG ig-like domain 5 (1945), excluding the MAG derivative MAG (dl-3)-FC, where the mutation reduces or eliminates the ability of the derivative to regulate neurite outgrowth as compared to endogenous or soluble MAG without eliminating binding to neuronal surfaces. The inhibitors of MAG are useful for promoting neural growth and regeneration. They are also useful for treating neural growth and regeneration. They are also useful for treating neural degeneration associated with injuries, disorders, or diseases. The disorder, disease, or condition is associated with expected with amylotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, kuntington's disease), or progressive supranuclear palsy. The present sequence represents the human NOGO-66 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy; neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
                                                                                                                                                                                                                                                                                                                            New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igd5), excluding the MAG derivative MAG (dl-3)-Fc, useful promoting neural growth and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a myelin-associated glycoprotein (MAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NSPLP protein coding sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 10; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGATAGCTTGGATCACACCCTTG 9
                                                                                                                                                                                                                   Cao Z;
                                         20-DEC-2002; 2002US-00327213.
                                                                                    20-DEC-2002; 2002US-00327213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US013469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00700607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV23697 standard; cDNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                   Filbin MT, Domeniconi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 72.0
nes 18; Conservative
                                                                                                                                                    (DOME/) DOMENICONI M.
(CAOZ/) CAO 2.
                                                                                                                                                                                                                                                            WPI; 2004-479666/45.
P-PSDB; ADR13968.
                                                                                                                             FILB/) FILBIN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9806841-A2
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24-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV23697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV23697,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                            New peptides that interact with myelin proteins Nogo, TNR and MAG, useful
in preparing a composition for treating CNS damage, spinal cord injury or
stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              describes perides which interact with the myelin proteins Nogor (specifically the Nogo-66 domain), the extracellular matrix glycoprotein tenascin-R (TN-R) (specifically TN-R epidermal growth factor like (TNR-BGFL) and myelin-associated glycoprotein (MAG). These proteins have phage display library exposed to a plate coated with the target protein. Peptides of the invention are useful in preparing a composition for treating central nervous system (CNS) damage, spinal cord injury or antigens. The peptides may also be used in vaccines against myelin antigens. The vaccine is based on the specific inhibitory portions of major myelin proteins, instead of the whole protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; gene; human; myelin-associated glycoprotein; MAG; neural growth; neural regeneration; apoptosis; amylotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes Nogo-66 domain b. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 12; Length 198; 72.0%; Pred. No. 0.079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "No start and stop codons given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple sclerosis; Creutzfeldt-Jacob disease; kuru;
multiple system atrophy; Lou Gehrig's disease;
progressive supranuclear palsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Pred. No. 0.07
ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 16; 81pp; English.
                                                                                                                                                 (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
(DENI/) DENISON C M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|||:|||:|||:|||:||||||||||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product= "NOGO-66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR13967 standard; cDNA; 198 BP
                                                               05-DEC-2003; 2003WO-GB005323
                                                                                                        06-DEC-2002; 2002US-0431620P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2004 (first entry)
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/*tag=
                                                                                                                                                                                                                                                            WPI; 2004-468811/44.
P-PSDB; ADQ16419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOGO-66 cDNA.
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                    24-JUN-2004.
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RESULT 10

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(INCY-) INCYTE PHARM INC.

US2004121341-A1

ADR13967/6

ID ADR13

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AC ADR13

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BB; g

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BB; g

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The present sequence is that of cDNA encoding human NOGO-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF90323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF90323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                      This sequence encodes a human neuroendocrine-specific protein-like protein (NSPLP) of the invention. Recombinant cells transformed with the DNA are used to express the NSPLP proteins, which are used to treat cancer and neurodegenerative diseases such as amyotrophic lateral sclerosis. Also antisense nucleic acids and antagonists of NSPLP can bused to inhibit activity of the NSPLP proteins. Antibodies specific for NSPLP are used for diagnosis and monitoring treatment of diseases associated with NSPLP expression, in usual immunoassays, and to isolate NSPLP from natural sources. The NSPLP proteins, or their fragments can also be used in drug screening to identify NSPLP antagonists. The mucleic acid can be used diagnostically and for monitoring treatment (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid can be used diagnostically and for monitoring treatment (in hybridisation or amplification assays); to isolate closely related sequences; in gene therapy for both sense and antisense applications (including use of ribozymes) and for mapping the natural genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; BST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                     Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 2; Length 261;
Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 261 BP; 62 A; 59 C; 56 G; 67 T; 0 U; 17 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards J, Duclert A, Lacroix B;
Hillman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST SEQ ID NO:137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CTGGATAGCTTGGATCACACCCTTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                Disclosure; Page 45; 73pp; English.
Goli SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX41193 standard; cDNA; 404 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
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Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-153778/13.
P-PSDB; AAY12360.
                                             WPI; 1998-159533/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409906548-A2
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Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX41193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                   disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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human secreted proteins, and encode the proteins given in AAX12261 to human secreted proteins, and encode the proteins given in AAX12261 to AAX12314, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, heamatopolesis regulating activity, chemoteration activity, heamatopolesis regulating activity, chemoteratical cartivity, nemeratoration/differentiation activity, nemeratoration activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products activity, respector/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products is can also be used for obtaining corresponding procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for almost in a proper activity is a polypeptide on the insertion of a content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 2; Length 404;
Pred. No. 0.088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 404 BP; 110 A; 75 C; 108 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Claim 1; Page 319; 824pp; English.
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24-JAN-2000; 2000GB-00001550.
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AAB82348). NOGO-C is a novel splice variant of the human NOGO gene on chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have previously been identified. The invention provides NOGO-C polypeptides and polymucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polymerleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzhaimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and dispnostic assays for detecting diseases associated with inappropriate NOGO-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;
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Gaps ö 4; Length 600; 0; Indels 100.0%; Score 25; DB 4; 72.0%; Pred. No. 0.093; rative 7; Mismatches 216 CTGGATAGCTTGGATCACACCCTTG 192 25 1 CUGGAUAGCUUGGAUCACACCCUUG Conservative Local Similarity Les 18; Conserv Query Match Matches

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BP ABN96987 standard; DNA; 639 13-AUG-2002 (first entry) ABN96987; RESULT 14

metastaric liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism. Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

Gene #3485 used to diagnose liver cancer.

Homo sapiens.

WO200229103-A2.

11-APR-2002

02-OCT-2001; 2001WO-US030589.

02-OCT-2000; 2000US-0237054P.

(GENE-) GENE LOGIC INC

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample. WPI; 2002-426119/45.

Vockley JG;

Peres-Da-Silva S,

Alvares C,

Horne D,

Claim 1; SEQ ID NO 3485; 298pp; English

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cytostatic ample. The method of the invention has hepatocropic, and cytostatic ample. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism. Note: The sequence data

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing cardiovascular disorders such as myocardial ischaemias; (d) wound healing (c) cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; se.
for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
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                                                                            Sequence 639 BP; 138 A; 114 C; 149 G; 147 T; 0 U; 91 Other;
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                    obtained in electronic format directly fr
ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                          ABL89601 standard; cDNA; 668
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SQ Sequence 668 BP; 164 A; 133 C; 167 G; 197 T; 0 U; 7 Other;

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1 CUGGAUAGCUUGGAUCACACCCUUG 25 |:|||:|||:|||:|| 430 CTGGATAGCTTGGATCACACCCTTG 406

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Search completed: July 30, 2005, 12:18:05 Job time : 309.446 secs

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Sequence 17 from Patent W00151520
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PAT 29-SEP-1999

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(Dases 1 to 404)

Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
5' EST of tissue-nonspecific secretory protein

Patent: JP 2001512011-A 131 21-AUG-2001;
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Bandman, O., Au-Young, J., Goli, S.K. and Hillman, J.L.
Polynucleotides encoding two novel human neuroendocrine-specific
                                         <1. _.>198
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ilarity 72.0%; Pred. No. 0.14;
Conservative 7; Mismatches
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AR028524
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JP 201512011-A/131
21-AUG-2001
31-JUL-1998 JP 2000505289
01-AUG-1997 US 08/905135
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JP 2001512011-A/131.
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                                                                                                                     /organism="synthetic construct"
|/mol_type="unassigned DNA"
|/db_xref="taxon:32650"
|/db_cref="cDNA encoding receptor binding inhibitor Pep2-41"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Peptides, antibodies thereto, and their use in the treatment of
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1 Similarity 72.0%; Pred. No. 0.14;
18; Conservative 7; Mismatches 0; Indels
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              Strittmatter, S.M.
Nogo receptor-mediated blockade of axonal growth
Patent: WO 0151520-A 17 19-JUL-2001;
YALE UNIVERSITY (US)
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Patent: WO 0151520-A 19 19-JUL-2001;
YALE UNIVERSITY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system damage
Patent: WO 2004052922-A 16 24-JUN-2004;
Singapore General Hospital Pty. Ltd. (SG)
Location/Qualifiers
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    .198
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Homo sapiens
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CQ827995/c
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PAT 27-AUG-2002

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/product="NOGO-C" protein"
/protein id="CAB99250.1"
/brotein id="CAB99250.1"
/db xref="GI:9408100"
/db xref="COA:09NGC3"
/db xref="COA:09NGC3"
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IGHVNCTIKELRARIET/UDDLVDSLKPAVLMWYFTYVGALFNGLTLLILLILLILLISLFSVPV
IYERHQAQIDHYLGLANKOVKDAMAKIQAKIPGKRKAE"
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Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 25; DB 6; Length 404;
Best Local Similarity 72.0%; Pred. No. 0.14;
Matches 18; Conservative 7; Mismatches 0; Indels
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Homo sapiens mRNA for Nogo-C protein (Nogo gene).
AJ251385
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/mol_type="mRNA"
/db_xref="taxon:9606"

    404
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

misc_feature 121..290
misc_feature 312..406
misc_feature 46..114
misc_feature 176..406
misc_feature 79..118
misc_feature 79..115
sig_poptide 132..257.
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Nogo gene; Nogo-C protein.
Homo sapiens (human)
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Michalovich, D.
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                                 CI2N15/09, C12N15/09, C07K14/47, C12Q1/68, C12N15/00, C12N15/00 CC
 JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO
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121. .225
26. .115
21. .353
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seq ASLFLLLSLTVFS/IV
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id T80234
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identity 99
region 200. .328
id AAl00508
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id AA100508
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id W68781
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OS Homo gapiens (human)
PN 7P 2002508182-A/45
PD 19-MAR-2002
PP 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/06551,09-REB-1998 US 60/074121 PR
BOUGUELERET, AYMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
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Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone
IMAGE:4291127), complete cds.
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 994)

Bougueleret,L., Declert,A. and Edwards,J.B.D.M.

Extended cDNA of secretory protein
Patent: JP 2002508182-A 45 19-MAR-2002;
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ilarity 72.0%; Pred. No. 0.15;
Conservative 7; Mismatches
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901. .906
979. .994.
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BD139293.1 GI:23234238
JP 2002508182-A/45.
Homo sapiens (human)
Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Unclassified.

1 (10 799)

Bandman, O., Au-Young, J., Goli, S.K. and Hillman, J.L.

Polynucleotides encoding two novel human neuroendocrine-specific
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/organism="Homo sapiens"
/or_type="unassigned DNA"
/db_xref="taxon:9606"
/noTe="EMBL/GenBank Accession No. W27023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                               639 bp Dl
Seguence 3485 from Patent WO0229103.
AX410838
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Extended cDNA of secretory protein.
BD139293
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/mol_type="unassigned DNA"
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Sequence 2 from patent US 5858708.
AR028522 GI:5940495
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                216 CTGGATAGCTTGGATCACACCTTG 192
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hes 18; Conservative
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BD249448 117-JUL-2003 Protein similar to neuroendrocrine-specific protein, and encoding
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                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 1122)
Michalovich, D. and Prinjha, R.K.
Protein similar to neuroendrocrine-specific protein, and encoding Patent: JP 2005522016-A 3 23-JUL-2002;
SMITHKLINE BEECHAM PLC
OS Homo sapiens (human)
PN JP 2002522016-A/3
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Protein similar to neuroendrocrine-specific protein, and encoding cDNA
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Christie,G., Michalovich,D., Simmons,D.L. and Walsh,F.S.
Inhibitor of neurite outgrowth in humans
Nature 403 (6768), 383-384 (2000)
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Homo sapiens mRNA for Nogo-B protein (Nogo gene).
AJ251384
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DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
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/organism="Homo sapiens"
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21-JUL-1999 JP 2000561310
22-JUL-1998 GB 9816024.
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Homo sapiens (human)
                                                                                                                                      BD249448.1 GI:33059218
JP 2002522016-A/3.
Homo sapiens (human)
Homo sapiens
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 21 Row: h Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="gynonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="MIM:664475"
/db_xref="MIM:664475"
/translation="MDGQKKNWKDKYVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIV
SVTAYIALALLSVTISFTIYGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
LGHYNCTIKELRALFLYDDLVDSLKFAYLMWFTYVGALFNGITLLILALISLEFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywineki, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identity to protein
This clone has the following problem: The cds is short compared to
the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-snyc.sramical.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                      Direct Submission
Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Fissue Procurement: CLONTECH
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Codon start=1
Product="reticulon 4, isoform C"
(protein id="AAH07109.1"
db_xref="GI:13937990"
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/clone_lib="NIH MGC_81"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:4291127"
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                                                                                                                                                                                   Strausberg, R.
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Best Local Simi
Matches 18;
                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                    PUBMED
REFERENCE
                                                                                                                                                                                                    TITLE
                                                                                                                                                                                   AUTHORS
                                                                                                               JOURNAL
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COMMENT
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                                                                    TITLE
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clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5902015
This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogf,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RIN-X"

/db_xref="LocusID:57142"

/db_xref="MIM:604475"
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LGHVNCTIKELRRLFLVDDLVDSLKPAVLMMVFTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
no hug 19, 2003 this sequence version replaced gi:12654418.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/codon_start=1
/product="reticulon_4, isoform C"
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Best Local Similarity 72.0%; Pred. No. 0.15
Matches 18; Conservative 7; Mismatches
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/db_xref="GI:12654419"
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/note="Vector: pOTB7"
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86 human secreted proteins.
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Klausner, R.D., Collins, F.S., Wagner, L., Schamen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schamen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.E., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.S., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="UniProt/Swiss-Prot:09NQC3"
/translation="MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEED
EDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERQPSWDPSPVSSTVPARSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWT
PPARPAPSTPAAPKRGSSGSVVDLLVWRDIKKTGVVPCASLFLLLSLTVFSIV
SVTAYIALALLSVTISFTYISFT YKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
LGHVACTIKELRRLELYDDLVDSLKPAVLMWYFTYVGALFNGLTLLILALISLESVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1151)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                       /product="Nogo-B protein"
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/db_xref="GOA:Q9NQC3"
                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                 Location/Qualifiers
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'gene="Nogo"
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Matches 18; Conser
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KEYWORDS
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                                 FEATURES
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HERRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER, PAUL YOUNG, JOHN PI M GREENE,
ANN M FERRIE,
COTH21/02, COTH21/04, C12N5/00, C12N5/04, C12N5/10, PC
COTH21/02, COTH21/04, C12N5/00, PC
C12N15/06, C12N15/00, PC
C12N15/09, C12N15/10, C12N15/11, C12N15/12, C12P21/04, C12P21/06 CC
Strandedness: Double;
C Topology: Linear;
CC Top
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60/058971 PR
60/058975 PR
60/060841 PR
60/060865 PR
60/061060 PI
                                                                                                                                                                                                                                         unidentified
unclassified.
l (bases 1 to 1213)
Moore, P.A., Shi, Y., Rosen, C.A., Ruben, S.M., Lafleur, D.W.,
Olsen, H.S., Ebner, R., Brewer, L.A., Young, P., Greene, J.M.,
Ferrie, A.M., Yu, G.L., Ni, J. and Feng, P.
Be human secreted proteins
Patent: JP 2002514990-A 78 14-MAY-2002;
HUMAN GENOME SCIENCES INC
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Location/Qualifiers
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13-JUN-1997 US 60/0495
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JP 2002514090-A/78
14-MAY-2002
                                                                         BD194907.1 GI:33004658
JP 2002514090-A/78.
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BGG20263 602618547
AU227299 AU227299
BX497992 DKEZ2D779M
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BMB2G161 K-EST0098
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BE694253 QV2-BT068
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Run

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library was prepared using the SMART cDNA library
construction Kit. (Clontech), doing only primer extension,
but not PCR amplification of the cDNA. The only deviation
from the published protocoll was that we cloned the cDNA
into a plasmid Vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 147)
Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paabo,S.
Selection on human genes as revealed by comparisons to chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB295964 linear EST 28-FEB-20
220010 rev 1 G08 r 056.abl Chimpanzee brain library Koos Pan
troglodytes CDNN-clone 220010 rev 1 G08 r 056.abl 5' similar to
human RTN4 neuroendocrine-specific protein C like (foocen), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Paabo S

Volutionary Genetics

Max-Planck-Institute for evolutionary Anthropology

Deutscher Platz 6, 04103 Leipzig, Germany

Tel: +49-(0)-341-3550 505

Fax: +49-(0)-341-3550 555

Email: paabo@eva.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
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                                                                  AA088462
BM826161
N55351
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CA389096
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AW995369
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AU297299
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W68688
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T81226 yd25a06.rl
AA100508 zn51c07.r
AA192599 zq01f08.r
AV729281 AV729281
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AW897156 CM0-NN005
BE169952 CM0-HT053
CD216746 EST S52 H
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BE763621 QV2-NT004
R96423 yq37f03.rl
AV725869 AV725869
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BEL69952 CMO-H7053
CD216746 EST S52 H
AA371486 EST S52 H
AA371486 EST S378
BER08007 QY1-BT663
CF125576 U1-HF-ELO
BU073029 im29406.9
E0311462 QY4-BNOO9
C14200 C14200 Clon
BF173127 WYE08564
CN429721 170006000
AA303835 EST16527
CD706840 EST23367
BE0078644 EST23367
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C14200 Clon
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                                                                                                                     July 30, 2005, 11:50:11; Search time 2561.15 Seconds (without alignments) 371.555 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     68479088
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               34239544 seqs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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AA371486
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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25
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9b_htc::*

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9b_est6:*:*

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EST 28-FEB-2003

T71810 yc62e07.rl BG896626 HOA47-1-G CB147989 K-EST0204 BF671862 602151760 AW995369 QV0-BN004

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Query Match

ઠે 셤 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AW897156

LOCUS

RESULT

REFERENCE AUTHORS

MEDLINE PUBMED JOURNAL

COMMENT

TITLE

FEATURES

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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0530-170
200-221-e07xt3=2000-02-17xt4=1)
Seq primer: puc 18 forward: 105
High quality sequence start: 105
High quality sequence stop: 201.

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Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
   EST 21-JUN-2000
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                         CMO-HT0530-170200-221-e07 HT0530 Homo sapiens CDNA, mRNA sequence.
BE169952. GI:8632673
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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mRNA
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Pred. No. 0.61;
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       201 bp
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CD216746.1 GI:30956721
EST.
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                                                                                                                                                                             Homo sapiens (human)
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Matches 18;
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/mol_type="mRNA"
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/dev_stef="taxon:9606"
/dev_steg="Adult"
/clone_lib="NN0056"
/note="forgan: nervous normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A Mini-library was made by cloning products
Site_2: Smal; A Mini-library was made by cloning products
Site_1: Ladvig Institute for Cancer Research)
No. 196,716 - Ludvig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                AW897156 176 bp mRNA linear EST 24-MAY-2000 176-NN0056-220400-341-£02 NN0056 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 176)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsonoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-NN0056-220 400-341-f02&t3=2000-04-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 176.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                        Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   100.0%; Score 25; DB 6; Length 147;
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                                    Pred. No. 0.58;
                         72.0%; Pred. ...
                                                                                                                                                                             147 CTGGATAGCTTGGATCACACCTTG 123
                                                                                                                                         1 CUGGAUAGCUUGGAUCACACCCUUG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW897156.1 GI:8061361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                    18; Conservative
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                            Best Local Similarity
Matches 18; Conserv
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Best Local Simi
Matches 18;
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Gaps

RESULT 3 BE169952/c

8 셤

ORIGIN

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9712 Medical Center Drive, Rockville, MD 20850
                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):175888"
/ba_xref="taxon:9606"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; 72.0%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 CTGGATAGCTTGGATCACACCCTTG 126
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                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
                         Tel: 3018699056
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Best Local Similarity
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BE080807/c
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                                                                                                                                                                                     FEATURES
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I (bases I to 257)

I (bases I to 257)

Adame, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Pitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.T., Kelley, J.W., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hatings, G.A., Hating, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wai, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Praser, C.M. and Venter, J.C., Yu, G.L., Ruben, S.M., Pischer, J., Pannon, M.R., Rosen, C.A., Haseltine, W.A., Pields, C., Praser, C.M. and Venter, J.C.
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EST83278 Prostate gland I Homo sapiens cDNA 5' end similar to
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                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="fibroblast"
|cell_line="2BS"
|dvv_stage="embryo"
|clone_line="thuman fibroblasts senescence upregulated
|subtracted_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
1 (bases 1 to 243)
Zhao,L., Zhang,Z. and Tong,T.

Expressed sequence tags from a human subtracted library, uprequlated in senescent fibroblasts
Unpublished (2003)
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Pred. No. 0.62;
7; Mismatches 0; Indels
                                                                                                           Contact: Zhao L
Department of Biochem and Molecular Biology
Peking University, Health Science Center
No.38, Xueyuan Road, Beijing 100083, P R China
Tel: 86 10 62091454
Email: to_zl@msn.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to tropomyosin, mRNA sequence.
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
72.0%; F
                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
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AA371486.1 GI:2023804
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Best Local Similarity 72...
The 18; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Loases 1 to 274)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@lodwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=@VI-BT0631-180 200-078-f05&t3=2000-02-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
High quality sequence story: 274.
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QV1-BT0631-180200-078-£05 BT0631 Homo sapiens cDNA, mRNA sequence.
BE080807
Fax: 3018699423
Email: arkerlav@tigr.org
Cor clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult, 21 yrs"
/clone lib="Prostate gland I"
/note="Organ: prostate; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 257;
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Gaps

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(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU073029
286 bp mRNA linear EST 27-AUG-2002 im29a06.yl Human insulinoma Homo sapiens cDNA clone IMAGE:6036371
5' similar to TR:Q9Y2Y7 Q9Y2Y7 FOOCEN-M. [2] TR:O94962 ;, mRNA
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Email: dmelton@biohp.harvard.edu
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
Email: dmelton@bio.go. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.
Location/Qualifiers

1. 286
1. 286
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Other ESTS: in2000.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 286)
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                                                                                              DB 7; Length 280;
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                                                                                                                                          72.0%; Pred. No. 0.64; iive 7; Mismatches
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//ilone="INMGE:3056281"
//ilone host="Unlug Tr phage resistant" |
//ilone lib="Unlug Tr phage resistant" |
//ilone lib="Unlug Tr phage resistant" |
//clone lib="Unlug Vector: pYX-Asc; Site I: EcoR I;
//clone lib="Unlug Vector: pyX-Asc; 
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8250
Eax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation. Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Lone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfil.html
Seq primer: pXx-5.
                   /clone lib="Br063"
//clone lib="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal, A min:-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF125576 280 bp mRNA linear BST 05-AUG-2003 UI-HF-ELO-avo-a-06-0-UI.r2 NIH MGC_212 Homo sapiens cDNA clone IMAGE:30563621 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Normalization and subtraction: two approaches to facilitate gene
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97044477
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/mol_type="mRNA"
/db_xref="taxon:9606"
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'dev_stage="Adult"
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SOURCE

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Gaps ..

DEFINITION ACCESSION VERSION

ORGANISM

KEYWORDS

REFERENCE AUTHORS

MEDLINE PUBMED COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Futheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 297)
1 (basea 1 to 297)
2 Pujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shimomiya, H., Takadi, A., Takada, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekwa, H., Shin, S. and Nakamura, Y.

1 Pujiwara et al. (1995)
2 Contact: Teutomu Fujiwara
2 Otsuka GEN Research Institute
3 Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan

Tel: 0886-65-2988
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Liubaio, J.O., Masih-Khan, B., Tang, H., Goncalves, J., Voralia, M., Li, Z.H., Nadeem, V., Cukerman, E., Franciso-Pabalan, O., Liew, C.C., A modecular compendium of genes expressed in multiple myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="GEN-037D12"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
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Concology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF173127 310 bp mRNA linear EST 23-1
MYE0856a Myeloma (MYE) cDNA library Homo sapiens cDNA, mRNA
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FORWARD: 5'-GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3'
BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seq primer: 5'-GAAATTAACCCTCACTAAAGG-3'.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CTGGATAGCTTGGATCACACCCTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CUGGAUAGCUUGGAUCACACCCUUG 25
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF173127
BF173127.1 GI:13439413
  EST.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                      Homo sapiens
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BF173127/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 288)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: breast normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                               BQ311462 289 bp mRNA linear EST 16-MAY-2002 QV4-BN0090-070600-249-g10 BN0090 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-BN0090-
070600-249-g10&ta3=2000-06-07&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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mol type="mRNA"
/db_xref="taxon:960s"
/dev_stage="Adult"
/clone_lib="BN0090"
                        CTGGATAGCTTGGATCACACCCTTG 127
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BQ311462.1 GI:20867010
EST.
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                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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/cell type="multiple myeloma"
/dev Stage="multiple myeloma"
/dev Stage="multiple myeloma"
/clone_lib="Myeloma (MYE) cDNA library"
/note="Vector: Lambda Zap Express; Site_1: ECORI; Site_2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(v]18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MNU reverse transcriptase. To protect the CDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32P]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
ECORI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The CDNAs were then
size-fractionated using Sephacryl 5-500 column and then
ligated into ECORI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using digapack
II packaging extract. The library had primary library
andomly selected for single pass sequencing."
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Contact: Brandenberger R
Regenerative Medicine
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 327)
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
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17000600012780 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
CN429721
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CN429721/c
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AA303835

BGT16527 Aorta endothelial cells, TNF alpha-treated Homo sapiens
CDNA 5' end similar to similar to neuroendocrine-specific protein
C, mRNA sequence.
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For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.igr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/orginism="Homo sapiens"
/mol type="mRNA"
/db_xref="ArCC (Inhost):115452"
/db_xref="type="force"
/db_xref="type="endothelial cell"
/dev_stage="adult"
/dev_stage="adult"
/clone lib="Aorta endothelial cells, TNF alpha-treated"
/note="forgan: aorta; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: XhoI"
                                   Gaps
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   7; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 328; 72.0%; Pred. No. 0.65;
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                   0; Indels
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Pred. No. 0.65;
7; Mismatches
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72.0%; F
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AA303835.1 GI:1956187
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Search completed: July 30, 2005, 15:00:58 Job time : 2564.15 secs
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1 (bases 1 to 346)
1 (bases 2 to 346)
1 (bases 2 to 346)
1 (bases 3 to 346)
1 (bases 3 to 346)
1 (bases 4 to 347)
1 (bases 6 to 347)
1 (bases 6 to 347)
1 (bases 7 to 348)
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QVO-BN0148-050500-215-d09 BN0148 Homo sapiens CDNA, mRNA sequence.
BE007854
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                                                                                                                                                                                                                                                                                                CD706840 342 bp mRNA linear EST 25-JUN-2003
EST23367 human nasopharynx Homo sapiens CDNA, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_risue type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTS generated from a normal nasopharynx CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 0.66;
7; Mismatches 0; Indels
      Indels
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Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn
                                                                                                                                                                                                                                                                                                                                                                                               CD706840.1 GI:32237470
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72.0%; F
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Contact: YiXin Zeng
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MEDLINE
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AUTHORS
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AUTHORS
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Once—"Organ: Breast normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2700402
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: Fax: +55-11
Fax: +57-11
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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100.0%; Score 25; DB 2; Length 346;
Best Local Similarity 72.0%; Pred. No. 0.66;
Matches 18; Conservative 7; Mismatches 0; Indels
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/mol_type="mRNA"
/mb_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0148"
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High quality sequence start: 17
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Location/Qualifiers
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CLONE: 28742
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Sequence 1, Appli
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Sequence 18, Appli
Sequence 16473, A
Sequence 24, Appl
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Sequence 117588,
Sequence 2, Appli
Sequence 3253, App
Sequence 106, App
Sequence 106, App
Sequence 14955, A
Sequence 14353, A
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Sequence 2285, Ap
                                                                                           (without alignments)
453.500 Million cell updates/sec
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                                                                             July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-3253

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US-09-949-016-14995

US-09-949-016-14995

US-09-949-016-14553

US-09-949-016-14553

US-09-676-6108-26

US-09-676-6108-26

US-09-715-249-1

US-09-715-249-1

US-09-949-016-16473

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US-09-949-016-17601
US-09-710-279-2285
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                                                                                                                                                                                                                             1202784 seqs, 818138359 residues
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Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
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3782, Ap
8294, Ap
25253, Ap
25253, A
25258, A
26286, A
31105, A
31106, A
82471, A
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Sequence 142013
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; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
    APPLICANT: Bandman, Olga
    APPLICANT: Au-Young, Janice
    APPLICANT: Au-Young, Janice
    APPLICANT: Hillman, Jennifer L.
    TITIE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
    TITLE OF INCENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
    MUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaccuticals, Inc.
    STREET: 3174 Porter Drive
    CITY: Palo Alto
    STATE: CA
    COUNTRY: U.S.
US-09-134-001C-1907
US-09-710-279-3782
US-09-621-976-16264
US-09-902-540-8294
US-09-949-016-25253
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US-09-949-016-124121
US-09-949-016-124121
US-09-949-016-124121
US-09-949-016-124121
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
       3046
3246
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TOPOLOGY: line
MOLECULE TYPE: cl
IMMEDIATE SOURCE:
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STATE: CA
COUNTRY: U.
ZIP: 94304
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Patent No. 6812339
GENERAL INFORMATION:
PAPLICANT: USTATE, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CL001307
CURRENT PAPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.0
                                                                                                                                                                                   FACENTE OF SELECTION OF SELECTION AND SELECTION AND USES THEREOF TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: 06/241,755
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHAND OF SEQ ID NOS: 207012
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Pred. No. 0.017;
Mismatches 0; Indels
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100.0%; Score 25; DE
Best Local Similarity 72.0%; Pred. No. 0.01
Matches 18; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Pred. No. 0.01
ive 7; Mismatches
336 CTGGATAGCTTGGATCACACCCTTG 360
                                                                                                                     US-09-949-016-117588
; Sequence 117588, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 72.04
Matches 18; Conservative
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US-09-949-016-117588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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RESULT 4

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US-09-949-016-3253/C

Sequence 3253, Application US/09949016
Factor No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE FEASTSEQ FOR Windows Version 4.0
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0.018;
| Sequence 2, Application US/08700607
| Patent No. 5858708
| GENERAL INFORMATION:
| APPLICANT: Bandman, Olga
| APPLICANT: Au-Young, Janice
| APPLICANT: Hillman, Olga
| APPLICANT: Hillman, Olga
| APPLICANT: Hillman Wonver HUMAN NSP-LIKE PROTEINS
| TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
| NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: INCYTE Pharmaccuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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; Pred. No. 0.018
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMUNICATION INFORMATION:
TELEPANE: 415-855-0555
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 7799 base pairs
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 CTGGATAGCTTGGATCACACCCTTG 266
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72.0%; E
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Best Local Similarity 72.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
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CLONE: Consensus
                                                                                                                                                                                                                                                                                                     Palo Alto
CA
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Tue Aug

LENGTH: 1669

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US-09-484-970B-106/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-949-016-14353
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; Sequence 382 Application US/09023655
; Patent No. 6607879
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; UNDER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STREE: CALIFORNIA
; COUNTRY: USA
                                                                                                                                    Gaps
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                                                                                             DB 4; Length 1669; 0.02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                    7; Mismatches
                                                                                             Score 25;
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                               |:|||:|||:|||430 CTGGATAGCTTGGATCACACCCTTG 406
                                                                                                                                                                         1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CUGGAUAGCUUGGAUCACACCCUUG 25
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TELEPAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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72.0%; P
                                                                                           100.0%;
72.0%; F
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Matches 18; Conservative
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nes 18; Conservative
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUNGNOT14
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; CLONE: 1508778
US-09-023-655-382
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IMMEDIATE SOURCE
                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253
                                                                                             Query Match
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Matches
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RESULT

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is Sequence 14995/C
; Sequence 14995, Application US/09949016
; Sequence 14995, Application US/09949016
; Sequence 14995, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TILLE OF INVENTION: WINGHER: 05/000-04-14
; PILOR REPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106
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100.0%; Score 25; DB 3; Length 4822;
Best Local Similarity 72.0%; Pred. No. 0.024;
Matches 18; Conservative 7; Mismatches 0; Indels
Sequence 106, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Walkeuth, Wayne
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT PELLING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24830 CTGGATAGCTTGGATCACACCCTTG 24806
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SOFTWARER PSECSEQ for Windows Version 4.0
SEQ ID NO 14995
LENGTH: 42075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3450 CTGGATAGCTTGGATCACACCCTTG 3426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.0
Matches 18; Conservative
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ORGANISM: Homo sapiens
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Deduced amino acid length of 381. Putative signal peptide Met-1 to Ala-24.
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Pred. No. 39;
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US-08-658-883B-1/c
Sequence 1, Application US/08658893B
Fatent No. 5708156
GENERAL INFORMATION:
TITLE OF INVENTION: An Epidermal Growth Factor
TITLE OF INVENTION: Receptor-like Gene Product and Its Uses
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESS: 3
STREET: 4206 Linden Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAPPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Biskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft DoS 6.2
SOFTWARE: Microsoft No. 5708156epad
CURRENT APPLICATION NUMBER: US/08/658,883B
FILING DATE: 31-MAY-1996
CLASSIFICATION NUMBER: No. 5708156 Applicable
PILING DATE: No. 5708156 Applicable
RICHARDATION NUMBER: No. 5708156 Applicable
REFERENCE/DOCKET NUMBER: No. 5708156 Applicable
REFERENCE/DOCKET NUMBER: No. 5708156 Applicable
REFERENCE/DOCKET NUMBER: No. 5708156 Applicable
TELEPONMULICATION INFORMATION:
TELEPONDMULICATION INFORMATION:
TELEPON
                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
   CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER PEG ID NOS: 182
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      828 GGACAGCTTGGATCACACTTTTG 806
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8%;
Best Local Similarity 65.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Western Springs
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STRANDEDNESS: Single
                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (245)...(1462)
US-09-676-610B-25
                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION:
OTHER INFORMATION:
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ZIP: 60558
                                                                                                                                                                                                                                  FEATURE
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FARCHAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 167886
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/02/1,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASELSEQ for Windows Version 4.0
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APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
IITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.4%; Score 18.6; D
64.0%; Pred. No. 51;
:ive 5; Mismatches
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| 132015 CTGGATAGCTGGGATCACAGGCATG 132039
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US-09-949-016-167886/c
; Sequence 167886, Application US/09949016
; Patent No. 6812339
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; Sequence 25, Application US/09676610B
; Patent No. 6444465
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Best Local Similarity 69.6°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-167886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Human
US-09-949-016-14353
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LENGTH: 175236
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JS-08-475-035-3/c
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                                                                                                                                                                                                                                                                   Sequence 26, Application US/09676610B
Fatent No. 6444465
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: OLICONUCLECTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 26
LENGTH: 1868
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                                            DB 1; Length 1868;
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APPLICANT: WOVARTIS AG
APPLICANT: VERES, GABOR
APPLICANT: VERES, GABOR
APPLICANT: PIPPIG, SUSANNE
TITLE OF INVERTION: selectable cell surface marker genes
FILE REFERENCE: 4-31192
CURRENT APPLICATION NUMBER: US 609/715, 249
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: us 60/166594
PRIOR APPLICATION NUMBER: us 09/539248
PRIOR PILING DATE: 2000-0330
NUMBER OF SEQ ID NOS: 16
SOUTHARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 3633
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Pred. No. 39;
5; Mismatches
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Pred. No. 44;
5; Mismatches
                                       Query Match 72.8%; Score 18.2; D
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches
                                                                                                                                                    1087 GGACAGCTTGGATCACACTTTTG 1065
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                                                                                                                            3 GGAUAGCUUGGAUCACACCCUUG 25
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Patent No. 6790614
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Best Local Similarity 65.2%;
Matches 15; Conservative
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Best Local Similarity 65.2%;
Matches 15; Conservative
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; NAME/KEY: CDS
; LOCATION: (504)...(1721)
US-09-676-6108-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                  RESULT 13
US-09-676-610B-26/c
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; ORGANISM: EGFR
US-09-715-249-1
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US-08-658-883B-1
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Sequence 3, Application US/08475035

| Sequence 3, Application US/08475035
| Patent No. 598553
| GENERAL INFORMATION:
| APPLICANT: KRAUS, WATTHIAS H.
| APPLICANT: KRAUS, WATTHIAS H.
| APPLICANT: AARONSON, STUART A.
| TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM TITLE OF INVENTION: GENE NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSES: ADDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: A patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/475,035
FILING DATE: 7 Jul 1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pertyman, David G.
REGISTRATION NUMBER: 1414.656
TELEPHONE: 404/688-0770
TELEPHONE: 404/688-0770
TELEPHONE: 404/688-070
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENERAR: FORTER SEQ ID NO: 3:
FUNCTH: 5532 base pairs
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Matches 15; Conservative
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STRANDEDNESS: single
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; LOCATION: 187..3816
US-08-475-035-3
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July 30, 2005, 11:00:21 ; Search time 731.757 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                    OM nucleic - nucleic search, using sw model
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	(without alignments) 1655.441 Million cell updates/sec
Title:	US-09-544-776-4
Sequence:	25 1 caacuucaggauuccagauaugccc 25

4708233 segs, 24227607955 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

9416466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmb1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AC124978 Mus muscu	AC127332 Mus muscu	AF065393 Homo sapi	AL929292 Zebrafish	AC025121 Homo sapi	AL391477 Human DNA	AC022378 Homo sapi	AY212597 Unculture	AB028866 Bos tauru	AX695905 Sequence	CQ861540 Sequence	AL008637 Human DNA	AL390204 Human DNA	Continuation (3 of	AP006116 Lotus cor	AC009157 Homo sapi	AF336797 Homo sapi	AC099511 Homo sapi	AC009071 Homo sapi
ID) AC124978) AC127332	AF065393	. AL929292	AC025121	AL391477	AC022378	AY212597	AB028866	AX695905	CQ861540	HS833B7	AL390204	AL672265 2	AP006116	AC009157	AF336797	AC099511	AC009071
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% Query Match Length DB	182405	230629	27745	218922	89317	150154	157280	1243	2423	40304	86574	86574	89566	110000	123325	151851	163217	173627	179168
% Query Match	83.2	83.2	81.6	80.8	79.2	79.2	79.2	77.6	76.8	76.8	76.8	76.8	76.8	76.8	76.8	76.8	76.8	76.8	76.8
Score	20.8	20.8	20.4	20.2	19.8	19.8	19.8	19.4	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.5
Result No.	1	0	ი ი	4	Ω Σ	y U	7	ω υ	0	c 10	c 11	c 12	13	c 14	c 15	16	c 17	18	19

ALIGNMENTS

Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submitted (20-4002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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5537. .5570

hote=single clone coverage"

552. .556

hote=*430 qual single clone coverage"

5175. .6317
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/rpt family="B2 Mm2"
complement (10594. .10701)
/rpt family="PB1"
11454. .11591
         1. .11787
/note="wags end_extension clone_end:SP6"
complement(655. .779)
/rpt_family="L2"
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complement(16149. .16316)
/rpt_family="B3"
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4234. .4269
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4559. .4606
/rpt_family="(TTTG)n"
4634. .4751
/rpt_family="1D3"
/rpt_family="1D3"
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/rpt_family="(GAAA)n"
6513. .6540
/rpt_family="AT_rich"
complement(7047. .7160)
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13477. 13668
/rpt_family="B2 Mm2"
complement(13930. 141!
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/rpt family="PB1D10"
5079. .5473
/rpt family="MTA"
5474. .6176
/rpt family="MTA"
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clone_end:8P6
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complement (1774. .187
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/rpt_family="(A)n"
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9384. .9421
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15933. .16065
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Submitted (19-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Hesearch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Anderson, M. Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, Y., Cooke, P., Cooke, P., Corum, B., Chang, J., Choepel, Y., Collymore, J., Cooke, S., Doodey, R., Dorris, L., Barickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N. Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T. Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Machen, C., Macdonald, P., Manjor, J., Manning, J., Matchews, C., Macdonald, P., Manjor, J., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Sewery, P., Roman, J., Schauer, S., Schubback, R., Seaman, S., Severy, P., Roman, J., Senues, J., Teefaye, S., Theodore, J., Soaman, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Voly, A., Wilson, B., Wul, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission, Whitshord Travers, M., Whison, B., Young, G., Zainoun, J., Zembek, L., Stamer, A., and Zody, M., Milson, B., Wul, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Schauer, A., And Zody, M., Direct Submission, M., Talama, T., Talama, M., T
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boughalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, Pierre, N., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartae, A., Kalls, C., Landers, T., Levine, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melurin, J., Mencus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vasilliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission, D., Young, G., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 13, 2004 this sequence version replaced gi:45268181.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@broad.mit.edu
------ Project_Information
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/organism="Mus musculus"
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/db xref="taxon:10090"
/chromosome="5"
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Center clone name: 107_D19
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Submitted (08-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 23, 2003 this sequence version replaced gi:27819587.
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Submitted (22-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases I to 230629)
MCPharson, J.D. and Waterston, R.H.
Direct Submission
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Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 230629)
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Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 230629)
McPherson,J.D. and Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 230629)

Nguyen, C., Cotton, M., Meyer, R. and Haglund, K.

The sequence of Mus musculus BAC clone RP23-13611

Unpublished (2001)
                                                                                                                                                                                                                                                                                                            Gaps
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Mus musculus BAC clone RP23-136I1 from 5, complete sequence
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Center code: WUGSC
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Contact: submissions@watson.wustl.edu
------ Summary Statistics
                          Center project name: M BA0136101
                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                    83.2%; Score 20.8; 70.8%; Pred. No. 29;
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3 (bases 1 to 230629)
McPherson, J.D. and Waterston, R.H.
Direct Submission
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Best Local Similarity 70.8
Matches 17; Conservative
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AC127332/c
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KEYWORDS
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION

g

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.resgen.com) or

This sequence is the entire insert of the clone. Location/Qualifiers NEIGHBORING SEQUENCE INFORMATION:

organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="5" . .230629

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 27745)

RS Gloeckner,G., Rosenthal,A. and Scherer,S.

Cosmid 1F1 of unknown origin containing G-binding protein

AL Unpublished

RS Gloeckner,G., Rosenthal,A., Drescher,B., Weber,J. and Schattevoy,R.

Intert Submission

AL Submitted (14-MAY-1998) Genome Analysis, Institut for Molecular

Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

CE 3 (bases 1 to 27745)

RS Gloeckner,G., Rosenthal,A., Drescher,B., Weber,J. and Schattevoy,R.

Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

AL Submission

AL Submission

AL Submission

AL Submission

AL Cacation/Qualifiers

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Ince | Location/Qualifiers

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| Mol Lype="genomic DNA" |
| Ab Eref="genomic DNA" |
| Ab Eref="genomic DNA" |
| Connolement (116 270)
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/note="BLASTN2 (EST exons), 1:1F1.X.599.00_Ex_3 8. .115 of
gb|C79823|C79823 Mus musculus 3.5-dpc blastocyst cDNA
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                                                                                                                                                                                                                                                                                                                                                                                           linear PRI 26-JUN-1998
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/evidence=not_experimental
/evidence=not_experimental
/evidence=not_experimental
/complement(1180. .269)
/note="BLASTN2" (EST exons), 5:1F1.X.599.00 Ex_1 229. .315
of gb|AA672091|AA672091 vl11f09.r1 Soares mouse mammary
gland NDMMG Mus musculus P = 9.9e-10 S = 350"
/evidence=not_experimental
/complement(307. .312)
/note="GenScan, score = 1.05%, comment = Length 6bp"
                                                                                                                                                                                                      Gaps
                                                                                                                                                                  Length 230629;
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0
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Homo sapiens cosmid 1F1, complete sequence.
AF065393. GI:3253311
                                                                                                                                                               DB 10;
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/rpt_family="AluSp"
complement(2148. .2298)
/evidence=not_experimental
/rpt_family="FRAM"
2175. .2282
                                                                                                                                                             score 20.8; DE Fred. No. 30; 5; Mismatches
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/evidence=not_experimental
/rpt_family="MIR"
1176. .1319
                                                                                                                                                                                                                                                                    208425 AACATCAGGATTCCAGGTATGCCC 208402
                                                                                                                                                                                                                                            2 AACTUCAGGAUUCCAGAUAUGCCC 25
              /rpt family="Alu"
36393. 36639
/rpt family="B4"
38541. 38756
/rpt family="L1"
39082. 39735
35276. .35411
                                                                                                                                                             Query Match 83.2%;
Best Local Similarity 70.8%;
Matches 17; Conservative
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VERSION
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SOURCE
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AF065393/c
LOCUS
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complement(17271. .17344)
/note="BLASTN2" (EST exons), 3:1F1.X.599.00 Ex_43 365. .438
of gb|AA224967|AA224967 nc34d12.r1 NCI_CGAP_Pr2 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 239
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                                                                                                                                                          TIEMQAITALAHLRAAVLYVMDLSEQCGHGLKEQLELFQNIRPLFINKPLIVVANKCD
VRRTTELSEBEDQXIFTDLQASEFPVLETSTLFTEGEVIQVYTKABADRLAHRVETFKNKG
NKYNSVLNRLHLAVPNKRDDKPMEVEVPYFRAQGFSVALEAVLEALIDQASKKITEL
CLPLPPSAGTKGVHHHLPERPPFIPEGVVARRKRMEIVEPRKKRERDLELEMGDDYIL
                                                                                                                                                                                                                                                                                                                                                      DLQKYWDLMNSSBKYDKIPEIWEGHNVADYIDPAIMKAKQIREKKKLKILLQSKEKNTQ
GPRMPRTAKKVQRADLENEMRSLGVDMDDKDNAHYAVQARRSRSVTRKRKREES"
                                                                   YGDSLYRCKQLKRAALGRMCTIIKRQKQSLEYLEQVRQHLSRLPTIDPNTRTLLLCGY
PNVGKSSFINKVTRADVDVQPYAFTTKSLFVGHMDYKYLRWQVVDTPGILDHPLEDRN
                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-not_experimental
13499. 113635_
horte="BLASTN2" (EST exons), 1:1F1.X.599.00_Ex_39_294. .430
of gp|AA438119] A4438119 vd22f07.s1 Knowles Solter mouse 2
cell Mus musculus cDNA P = 6.7e-21 S = 595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1422/. | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 1420| | 142
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/note="BLASTN2" (EST exons), 2:1F1.X.599.00 Ex_41 143.
of gb|AA209775|AA209775 mo79a08.rl Beddington mouse
embryonic region Mus musculus P = 1.1e-14 S = 459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="BLASTN2 (EST exons), 2:1F1.X.599.00 Ex 43 247. of gb|AA209775|AA209775 mo79a08.rl Beddington mouse embryonic region Mus musculus P = 7.4e-23 S = 640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(17270. 17344)
/note="BLASTN2 (EST exons), 4:1F1.X.599.00_Ex_43_365.
of gb|AA2255040|AA225040 nc34c01.r1 NCI CGAP_Pr2 Homo
sapiens CDNA clone P = 5.0e-07 S = 288"
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complement(17270. .17344)
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RLSQILTDFPFKLDDIHPFYADLMNILYDKDHYKLALGQINIAKNLVDNVAKDYVRLMK
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Region: CpG island"
/evidence=not_experimental
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'note="GenScan, score = 1.05%, comment = Length 6 bp"
                                                                   = 1.6e-10 S = 363"
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/note="TN1000 insertion site in cosmid 1F1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |3047 .4329
|note="111 with 88% homology to 112"
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3'-end sequence, similar P = /evidence=not_experimental complement(3368. .3460) /evidence=not_experimental /rpt_family="MER72"
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/evidence=not_experimental
/rpt_family="AluJ/FLAM"
6364. . 6448
/evidence=not_experimental
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complement (7215. . 7388)
/evidence=not_experimental
/rpt_family="RAM"
7745. 8359
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complement (4554. .4670)
/evidence=not_experimental
/rpt_family="AluSp"
4854. .4886
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/rpt_family="FRAM"
complement (4090. .4160)
/evidence=not_experimental
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4214. .4303
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4525. .4550
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/rpt_family="AluSc"
43047.4329
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'db_xref="GI:3153873"
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Gaps

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Danio rerio

VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

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ACCESSION

Johnson, C

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

FEATURES

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Dipublished

Signature, Musbaum, C., Lander, E., Abraham, H., Allen, N., Bairen, S., Bladdain, J., Barra, N., Bastien, V., Beda, F., Baldwin, J., Barra, N., Barket, G., Barket, G., Campopiano, A., Castle, A., Cheepel, Y., Colangelo, M., Collins, S., Campopiano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancoque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McKernan, K., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vonsilley, H., Viel, R., Vola, A., Milson, B., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Direct Subnission.
                                                                                                                                                                                                                                                                                                                                                                                         ACO25121 89317 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 1 clone RP11-21M14 map 1, LOW-FASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 89317) Nusbaum, C. and Lander, B. Linton, L., Nusbaum, C. and Lander, B. Homo saplens chromosome 1, clone RP11-21M14
                                                        Length 218922;
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                              Indels
                                                                                                                           <u>ب</u>
                                                               DB 5;
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                                                            Score 20.2; D
Pred. No. 60;
5; Mismatches
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Center clone name: 21_M_14
                                                                                                                                                                                           1 CAACUUCAGGAUUCCAGAUAUGCCC
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AC025121.1 GI:7158932
                                                               80.8%;
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                                                                                                                           17; Conservative
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                                                               Query Match
Best Local Similarity
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AUTHORS
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AUTHORS
                                                                                                                              Matches
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KEYWORDS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at from a Sebrafiab BAC library verwor. Traincent.
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                                                                                                                                                                                                                                                                                                                                                                                         VRT 23-SEP-2003
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Clone-derived Zebrafish pUC subclones occasionally display
Clone-derived Zebrafish pUC subclones occasionally display
Clone-derived Zebrafish pUC subclones occasionally display
Conserved TA repeats. Where this is found the longest good quality
representation will be submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhirong Bao and Sean Eddy, submitted), and those
beginning 'drr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostel; Ostariophysi, Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 1SA, UK. E-mall enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@snger.ac.uk on Sep 23, 2003 this sequence version replaced gi:28445772.
                                                                                                                                                                                                                                                                                                                                                              ALY29292 218922 bp DNA linear VRT 23-5EP-200
Zebrafish DNA sequence from clone DKEY-11L24 in linkage group 14,
                                                                                                Gaps
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                              Length 27745;
                                                                                             1; Indels
                                 DB 9;
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                              Score 20.4; D
Pred. No. 43;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/db_xref="taxon:7955"
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/clone_lib="DanioKey"
                                                                                                                                                                                              6933 ACTTCAGGATTCCAGATATGTC 6912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
                              Query Match 81.6%;
Best Local Similarity 68.2%;
Matches 15; Conservative
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f 854	of 860	840 1	10 pp	998 J	00 bp	00 bp	dq oc	E 868	855	00 bp E 861	dq 00	00 pp	E 874	839	30 bp	dq oc	: 853 00 pp	867	20 DE	00 bp	ф 00	38 35 30 35	877	10 pp	00 bp	d Q	872 30 bo	847	969 1	00 bp	00 bp	7, 0, odd	874 00 bp	873	967 1	00 bp	00 bp	00 bp	70 pb	70 pb	879 30 bb
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d. 854: 0	1814:	2754:	3711:	4677:	4777: 5649:	5749:	6664:	7532:	8487:																																
preserved	955	1915	2855	3812	4678	5650	6565	6665	7633	8488 8588	9449	10415	10515	11489	12328	13289	13389	14342	15309	16153	17071	17171 ·18066	18166	19143	20004	20958	21058 21930	22030	22977	23846 23946	24813	25785	25885 26759	26859	27832	28699 28799	29663 29763	30640	31571	32533	32633 33512
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14497 144597 144

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AC022378 15-0CT-2000 Homo sapiens chromosome 3, WORKING DRAFT SEQUENCE, 13 unordered
                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 157280)
Dong,H., Zhang,C., Lin,W., Wan,M., Xu,S., Gu,W., Tu,Y., Jia,J.,
Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-FEB-2000) Genomic Dept., Chinese National Human Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai, Shanghai 201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shanghai 201203, P. R. China
On Sep 26, 2000 this sequence version replaced gi:6862622.
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8876 contig of 6174 bp in length
690 of 6174 bp in length
990 of winnown length
13133 contig of 6174 bp in length
13183 contig of 4257 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
3410; contig of 5662 bp in length
gap of unknown length
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gap of unknown length
79394: contig of 12285 bp in length
gap of unknown length
95402: contig of 16008 bp in length
gap of unknown length
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/organism="Homo sapiens"
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                                                                                                                                                                                                      AC022378.2 GI:10305057
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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/clone_lib="83b2"
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KEYWORDS
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                                                                                                                  DEFINITION
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                                                            AC022378
LOCUS
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Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

NumqueryGeanger.ac.uk Clone requests: clonerequestGeanger.ac.uk
On Jul 19, 2002 this sequence version replaced gi:21337432.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RPI1-21M14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: PBAce3.6
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                                                                                                                                                                              AL391477 150154 bp DNA linear PRI 17-JUL-2002
Human DNA sequence from clone RP11-21M14 on chromosome 1, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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13870 AACTTCAGGATTCCAGAAATTCC 13848
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AL391477/c
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/product="prolyl oligopeptidase"
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AQNKITVPFLEQCPIRGLYKERMTELYDYPKYSCNFKKGKRYFYFYNTGLQNQRVLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                     ODSLEGGRARVCLDPNTLSDDGTVALRGYAFSEDGEYVAYGLSASGSDWVTĪKFWKVDG
AKELADVLESTVKFSCMAMGARGMFYNAYPQDGASBOGTESTNLLAGVCLYHTJGTD
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LKWVKLIDNPEGEYDYVTNEGTVFTFKTNRHSPNYRLINIDPTDEESRWKVLVPEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYGETWHKGGILANKQNCFDDFQCAABYLIKEGYTSPKRLTINGGSNGGLLVATCANQ
RPDLFGCVIAQVGVMDMLKFHKYTIGHAWTTDYGCSDNKQHFEWLIKYSPLHNVKLPE
ADDIQYPSMLLLTADHDDRVVPLHSPKFIATLQHLVGRSRKQNNPLLIHVDTKAGHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDVLEWVACVRSNPIVJCYLHDVKNTLQLHDMATGALLKTPPLEVGSVVGYSGQKKDT
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PMFIVHKKGIKLDGSHPAFLYGYGGFNISITPNYSVCRLIFVRHMGGVLAVANIRGGG
Submitted (10-JUN-1999) Teutomu Kabashima, School of Pharmaceuti Sciences Nagasaki University, Department of Biotechnology; 1-14 Bunkyo-machi, Nagasaki, Nagasaki 852-8521, Japan (E-mail: -kabashima@cc.nagasaki-u.ac.jp, Tel:81-95-847-1111 (ex.2522), Fax:81-95-843-2444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 19.2; DB 4; Length 2423; 66.7%; Pred. No. 1.6e+02; ive 5; Mismatches 3; Indels 0;
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Sequence 1532 from Patent WO03008583.
AX695905
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Novel compositions and methods for canc
Patent: WO 03008583-A 1532 30-JAN-2003,
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/db_xref="taxon:9606"
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                                                                                                                                         1. . 2423

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_lib="brain"

120. . 2252

/EC_number="3.4.21.26"
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Best Local Similarity 66.7
Matches 16; Conservative
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Best Local Similarity
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AX695905/c
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Simpson, J.M., Santo Domingo, J.W. and Reasoner, D.J.
Assessment of equine fecal contamination: the search for alternative bacterial source-tracking targets
alternative bacterial source-tracking targets
FEMS Microbiol. Ecol. 47 (1), 65-75 (2004)
2 (bases 1 to 1243)
Simpson, J.M., Santo Domingo, J.W. and Reasoner, D.J.
Direct Submission
Sibmitted (08-JAN-2003) Office of Research and Development - Water Submitted (08-JAN-2003) Office of Research and Development - Water Supply Water Resources Division, U.S. Environmental Protection
Agency, 26 W. Martin Luther King Dr., Cincinnati, OH 45268, USA
Location/Qualifiers
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Bos taurus mRNA for prolyl oligopeptidase, complete cds.
AB028866
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                                                                                                                                                                                 BCT 16-JAN-2004
                                                                                                                                                                                    AY212597
Uncultured bacterium clone 146d820 16S ribosomal RNA gene, partial
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Yoshimoto, T., Miyazaki, K., Haraguchi, N., Kitazono, A., Kabashima, T.
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Yoshimoto,I., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,I.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/organism="uncultured bacterium"

/mol_type="genomic DNA"

/isoTation_source="water 20 m downstream of manure"

/db_xref="taxon:77133"

/clone="146ds20"
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77.6%; Score 19.4; DB 1;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 15; Conservative 5; Mismatches 1;
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/product="16S ribosomal RNA"
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                                                 22869 AACTTCAGGATTCCAGAAATTCC 22891
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| CTTCAGGATTCCAGACATGCC 981
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AY212597.1 GI:37786996
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                                                                                                                                                                                                                                                                                                                        uncultured bacterium uncultured bacterium
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 19.2; DB 6; Length 40304; llarity 66.7%; Pred. No. 1.8e+02; Conservative 5; Mismatches 3; Indels 0;
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Tue Aug

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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 happing Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22

IMPORTANT: This sequence is not the entire insert of clone CTA-83387 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone CITF22-24E5 is at 100 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1233. .1462)
/note="L2 repeat: matches 2418. .2653 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642..653
Chote="4.0 copies 3 mer AGA 24% conserved"
Chote="4.0 copies 3 mer AGA 24% conserved"
Chote="MIR repeat: matches 212..254 of consensus"
Inote="2.1084"
Inote="2.6 copies 5 mer GGAGA 26% conserved"
Inf3..173
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/note="AluSx repeat: matches 1. .307 of consensus"
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//note="MLT1J repeat: matches 1. .261 of consensus"
complement (4.4555)
//note="MIR repeat: matches 64. .143 of consensus"
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complement(4645. .5195)
/note="LTR50 repeat: matches 4. .766 of consensus"
5291. .5370
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/note="2.0 copies 8 mer GAGGAAGG 32% conserved"
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'note="2.5 copies 6 mer CCCGCC 30% conserved"
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note="2.0 copies 5 mer GAAAA 20% conserved"
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/note="2.2 copies 5 mer GGGAT 22% conserved"
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/note="4.2 copies 4 mer CTCC 25% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5 copies 4 mer TCCC 20% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139. .258
'note="20.0 copies 1 mer C 22% conserved"
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  feb site: http://www.sanger.ac.uk
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/clone="CTA-833B7"
/clone lib="CIT978SK-A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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/db_xref="taxon:9606"
                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome="22"
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/note="2.1 c
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/note="2.5 c
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/note="2.5
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Cambridgeshire, CBN 18A, Wr. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 18, 198 this sequence version replaced gi:2578146.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSEROT; Tr:, TREMBL; Wp:, WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C elegans/wormpep CTA-833B7 is

from the human BAC library described in U-J. Kim et al. (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                        PAT 10-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS833B7 B6574 bp DNA linear PRI 05-JUN-2003 Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CFSTB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTB, STSB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                           Burczynski,M., Twine,N., Dorner,A.J. and Trepicchio,W.L.
METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
Patent: WO 2004072265-A 173 26-AUG-2004;
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)
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Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
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HTG; colony stimulating factor; CSF2RB; cytosolic neutrophil
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                                                        linear
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                                                        CQ861540 86574 bp DNA Seguence 173 from Patent WO2004072265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                         CQ861540
CQ861540.1 GI:51982529
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VECTOR: pBeloBAC11
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Homo sapiens (human)
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RESULT 11
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HS833B7/c
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.313 of consensus"

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jóin(11913. 12573,15415. 15499,16289. 16442,18762. 18832,
21785. 21912,23022. 23079,23697. 23795,27023. 27153,
27399. 27464,28998. 29288)
                                                                                                                                                                                                                                                                                                                                                                                                                                7047. .7193 '
/note="6.1 copies 24 mer GTGTGCATGTGTATATGTGCCTGC 113%
                                                            .677. .6268
'note="L1MR1 repeat: matches 5604. .6332 of consensus"
                                                                                                                                                                                  . 6962
/note="2.1 copies 14 mer TGCATGTATGTGCA 49% conserved"
                                                                                                                                                                                                                                                                                                                              2 copies 14 mer GTGTATATGTACAT 66% conserved"
                                                                                                                                                               note="MER115 repeat: matches 393. .688 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="match: cDNAs: Em:AB002665 Em:X77094 Em:U59488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7033. .7332

note="L2 repeat: matches 3165. .3313 of consensus"

7333. .7342

note="2.5 copies 4 mer GAAT 20% conserved"
                                                                                                                        .2819 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7253 . 8341
note="L2 repeat: matches 3214, .3311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="2.2 copies 5 mer TTTCA 22% conserved" complement(11386. .11858) /note="12 repeat: matches 2722. .3312 of consensus" 11913. .29288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.347. 7532

/note="MIR repeat: matches 2. .191 of consensus"

complement (7537. .7440)

/note="MIR repeat: matches 158. .262 of consensus"

complement (8152. .8228)

/note="MIR repeat: matches 184. .260 of consensus"
                                      note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                       .9 copies 10 mer TGCAGGTGTG 29% conserved"
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Em:AA465389 Em:AA485518 Em:AI381940 Em:AA744805
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'note="2.1 copies 8 mer TGTACATG 25% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7048. .7080
Ynote="5.5 copies 6 mer TGTGTA 30% conserved"
7053. .7085
Ynote="4.1 copies 8 mer ATGTGTAT 29% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9920. .9935
/note="2.0 copies 8 mer TTGGGGGG 32% conserved"
10303. .10313
                                                                                                                                                                                                                                                                                                                                                 7000. .7014 Totes 6 mer TGTACA 30% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1125. 7136
'note="2.0 copies 6 mer ATGTGT 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148. .7164 notes 6 mer TGTGTA 25% conserved"
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note="2.5 copies 4 mer TGCA 20% conserved"
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/note="L1ME1 repeat: matches 5523.
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                                                                                                6302. .6481
/note="L2 repeat: matches 2636.
complement(6483. .6755)
                 .5676)
                   complement (5371
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/note="6.2 co
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/note="2.5 cc
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/note="5.0 cc
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/note="2.0 co
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Unified Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Consequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: En; EMBL; Sw;, SWISSEROT; Tr:, TREMEL; Well: Welley Williams or the WormPep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, the sanger centing can be found at the contract of bacterial clone at the contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, the sanger centing at the contract of t
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Em:AA975113 Em:AA969460 Em:AA948430 Em:AI435296
Em:AI299103 Em:AA648472 Em:AA702857 Em:AI088359 Em:D20144
Em:AA909156 Em:AA688071 Em:W95229 Em:AI439568"
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RP11-196D4 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                          join(12542. .12573,15415. .15499,16289. .16442,18762. .1
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29193)
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                                                                                                                /evidence=not_experimental
complement(11982. .12109)
/note=="L2 repeat: matches 2918. .3064 of congensus"
12358. .12367
/note=="3.3 copies 3 mer GGA 20% conserved"
/note=="2.2 copies 5 mer GAGAC 22% conserved"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 89566)
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/codon_start=1
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AL390204
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Gaps

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                     Location/Qualifiers
1. 123325
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                                                                                                                                                                                                                                                                                                                                                                                                   25756 CAACTTCAGGATTCAAGATAATCC 25733
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Job time : 736.757 secs
        Fax:81-438-52-3934)
                         FEATURES
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sections only once, except for a short overlap.
The true left end of clone RP11-196D4 is at 1 in this sequence. The true left end of clone RP11-307C12 is at 87567 in this sequence.
Location/Qualifiers
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DDA Res. 10 (1), 27-33 (2003)
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Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
Submittent of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids I; Fabales; Fabaceae, Papilionoideae; Loteae,
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Lotus corniculatus var. japonicus genomic DNA, chromosome 1, clone:LjT40C04, TM0199, complete sequence.
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1 Similarity 66.7%; Pred. No. 1.9e+02;
16; Conservative 5; Mismatches 3;
                                                                                      1. .89566
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/clone="RR11-196D4"
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Fragment Name Begin En
AL672265 0 100001 21
AL672265 2 200001 31
AL672265 3 300001 41
AL672265 4 400001 51
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AP006116.1 GI:29122755
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Continuation (3 of 6)
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AL672265 2/c
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

July 30, 2005, 10:32:26; Search time 308.446 Seconds (without alignments) 479.804 Million cell updates/sec

Title:

US-09-544-776-4 25 Perfect score:

1 caacuucaggauuccagauaugccc Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB.seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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geneseqn2003cs:*
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geneseqn2004as:*
geneseqn2004bs:* geneseqn2002as:*geneseqn2002bs:*geneseqn2003as:*geneseqn2003bs:* geneseqn2001bs:* geneseqn2001as:* geneseqn1990s:* geneseqn2000s:* geneseqn1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aac64408 Human Nog	Abl70775 Corn tass	Ada03014 Human NCF	Adb72752 Human NCF	Adc85494 Human Ncf	Adm74609 Human car	Abk83560 Human cDN	Adr52822 Drug ther	Abx43504 Bovine ES	Abx45854 Bovine ES	Abx40707 Bovine ES	Aak86539 Human imm	Continuation (11 o	Aax25487 Human myo	Abl02346 Drosophil	Abl26458 Drosophil	Ach21863 Human adu	Aak94059 Human cDN	Adl30486 3' end of	Aak63128 Human imm
SUMMARIES	ΩI	AAC64408	ABL70775	ADA03014	ADB72752	ADC85494	ADM74609	ABK83560	ADR52822	ABX43504	ABX45854	ABX40707	AAK86539	AAT42063 10	AAX25487	ABL02346	ABL26458	ACH21863	AAK94059	ADL30486	AAK63128
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	& Query Match	100.0	76.8	76.8	76.8	76.8	76.8	76.8	76.8	74.4	74.4	74.4	74.4	74.4	73.6	72.8	72.8	70.4	70.4	70.4	70.4
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Abl21915 Drosophil Aac59134 Human sec Adq25167 Human sof Aai14791 Probe #47	Human Probe Human	Frobe Human Human Human	Aai04584 Probe #45 Abs0473 Human gen Aaq98543 Prolyl en Acc49473 Human pro	Ade38352 Human pro Adr40162 Human pro Adb62183 Human cDN Adg89414 Cancer de	Abl21914 Drosophil Abl21916 Drosophil Aa803072 Human dia Aa106639 Human rep Aas40722 DNA encod Adj09928 Human pro
4 ABL21915 3 AAC59134 12 ADQ25167 4 AAI14791	4 ABA56518 4 AAI36149 4 ABA45986	4 ABA26148 4 AAK30186 4 AAK04674 4 ABS29836	5 AA104584 6 ABS04773 2 AAQ98543 8 ACC49473	10 ADE38352 13 ADR40162 10 ADB62183 10 ADG89414	4 ABL21914 A BAL21916 4 AAL06639 5 AAS40722 11 ADJ09928
1362 1379 1441 1994	1994	1994 1994 1994	1994 1994 2130 2562	2562 2562 2712 2756	3362 3923 4744 19696 19696
70.4 70.4 70.4	4.07	4.4.4.4	70.4 70.4 70.4	4.07	4.07 4.07 4.07 4.07 4.07
17.6 17.6 17.6 17.6	17.6	17.6	17.6 17.6 17.6 17.6	17.6 17.6 17.6	17.6 17.6 17.6 17.6 17.6
22 23 24 24	C 25 C 26 C 27	C 28 C 30 C 31	0 0 0 0 0 3 3 3 3 4 4 3 3 5 3 4 4 5 5 5 5 5 5 5 5	0 36 37 38 38	0 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

Human, Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; antisense; Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4. BP. AAC64408 standard; RNA; 25 (first entry) 08-FEB-2001 AAC64408; RESULT 1 AAC64408 X1211X8X8X8X8X8X8X8X11114X8X8X6X6X6X6X6X6X8X

Location/Qualifiers phosphorothioate; ss. Homo sapiens

1. .25 /*tag= a /note= "phosphorothioate linkages" Key modified_base

WO200060083-A1

12-OCT-2000.

07-APR-2000; 2000WO-US009383

99US-0128372P. 99US-0140331P. 08-APR-1999; 21-JUN-1999;

(CHIR) CHIRON CORP.

Williams LT; Halenbeck R, Wei D,

WPI; 2000-665007/64.

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, qualty and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid

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Gaps

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Indels

3;

Score 19.2; DB 6; Length 270; Pred. No. 40;

Query Match 76.8%; Score 19.2; D Best Local Similarity 62.5%; Pred. No. 40; Matches 15; Conservative 6; Mismatches

2 AACTUCAGGAUUCCAGAUAUGCCC 25

Sequence 270 BP; 61 A; 46 C; 65 G; 98 T; 0 U; 0 Other;

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                       The present invention describes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynuclectides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligomucleotide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
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                                                                                                                                                                                                                                        Sequence 25 BP; 7 A; 8 C; 4 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                 1 CAACUUCAGGAUUCCAGAUAUGCCC 25
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Claim 25; Page 32; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL70775 standard; cDNA; 270 BP.
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Matches 25, Conservative
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(ITOL/) ITO L Y.
(SHER/) SHERMAN B K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL70775;
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protoconcogenes. The CA nucleic acid sequences can be used to diagnose
                                                                                                                                                                                                                                                                 Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                           Human NCF4 carcinoma associated gene, SEQ ID NO:1532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1532; 245pp; English.
ADA03014 standard; DNA; 40304 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2001; 2001US-00035832.
                                                                                                                                                                                        06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                                                                                                                   WO2003057146-A2
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                    ADA03014;
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                                                                                            ADA03014/c
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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable

Claim 1; SEQ ID NO 149; 201pp; English.

37678 AACTTGAGGATGCCAGATATTCCC 37655

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2 AACTUCAGGAUUCCAGAUAUGCCC 25

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carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                             Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;
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                                                                                                                                                                                                                               Length 40304;
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                                                                                                                                                                                                                                   DB 9;
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                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                               Score 19.2;
Pred. No. 82;
                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 580; 2304pp; English.
                                                                                                                                                                                                                                                                                                                         37678 AACTTGAGGATGCCAGATATTCCC 37655
                                                                                                                                                                                                                                                                                                       2 AACTUCAGGAUUCCAGAUAUGCCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                ADB72752 standard; DNA; 40304 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
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30-NOV-2001; 2001US-00997722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-2001; 2001US-00034650
                                                                                                                                                                                                                               Match 76.8%;
Local Similarity 66.7%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NCF4 gene
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Cytostatic, gene therapy, vaccine, cancer, carcinoma-associated gene, CA, secreted, transmembrane, intracellular, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                any of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant nucleic acid comprising a nucleotide sequence of ar
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 280; 983pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AACUUCAGGAUUCCAGAUAUGCCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC85494 standard; DNA; 40304 BP
                                                                                                                                                                                                                                                                         02-DEC-2002; 2002WO-US038582
                                                                                                                                                                                                                                                                                                       30-NOV-2001; 2001US-00997722
                                                                                                       Human Ncf4 genomic sequence.
                                                                         (first entry)
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Best Local Similarity
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                                                                                                                                                                                  Homo sapiens.
                                                                         01-JAN-2004
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                                            ADC85494;
ADC85494/c
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Matches
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Gaps

Query Match 76.8%; Score 19.2; DB 10; Length 40304; Best Local Similarity 66.7%; Pred. No. 82; Mismatches 16; Conservative 5; Mismatches 3; Indels 0;

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Homo saptens.

WE US2004072154-A1.

WE US2004072154-A1.

WE US2004072154-A1.

WE US2004072154-A1.

WE US2004072154-A1.

WE US200012 2000US-00747377.

WE 22-DEC-2000; 2000US-00747377.

WE 23-DEC-2000; 2000US-00747377.

WE 23-DEC-2000; 2000US-00747377.

WE 24-DEC-2000; 2000US-0074737.

WE 24-DEC-2000; 2000US-0074737.

WE 24-DEC-2000; 2000US-0074737.

WE 24-DEC-2000; 2000US-0074737.

WE 24-DEC-2000; 2000US-007473.

WE 24-DEC-2000US-007473.

WE 24-DEC-2000
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Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other; Query Match 76.8%; Score 19.2; DB 12; Length 40304; Best Local Similarity 66.7%; Pred. No. 82; Answatches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

2 AACUUCAGGAUUCCAGAUAUGCCC 25 |||::||||:|||||:||||| 37678 AACTTGAGGATGCCAGATATTCCC 37655

8 8

RESULT 7 ABK83560/c ID ABK83560 standard; CDNA; 86574 BP.

ABK83560;

14-AUG-2002 (first entry)

Human cDNA differentially expressed in granulocytic cells #131.

Human; se; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; aglomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

T WEN 2002 :

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

3eazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 131; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC MR chip analysis as given in the specification, and comparing the expression level in an unactivated GC, where captured an expression level in an unactivated GC, where captured at least one grae in Gs; indicative of GCA. Also included are differential expression of Gs is indicative of GCA. Also included are modulating (M2) aby contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of pathogen or sterile inflammatory disease, by detecting the level of captusors of the gene is indicative of inflammation; (4) treating cresponse in a subject, exposure of a subject to a pathogen or sterile inflammation of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating cresponse in a subject, exposure of a subject to a pathogen or sterile inflammation of gene(s) from Gs, where the level of expression of the gene(s) from Gs, where the level of expression of the gene(s) from Gs, where the level of expression of the subject, of a subject, exposure of a subject, exposure of a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a subject to a pathogen or sterile inflammation in a tissue, an allergic response in general sequence of a subject to a pathogen or sterile inflammation in disease, of cardiac reperfusion injury, real repertual disease, locarative colitis, parasitic infection, parasitic infection para of the priname inflammation in a tissue will disea

Gaps

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Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;
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ID RAD52822/C

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ADR52822;
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ADR52822;
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ADR52822;
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IB-NOV-2004 (first entry)
XX

Gruy activity monitoring; expression peripheral blood sample; peripheral curry)
XX

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HORD Sapiens.
XX

HOMO Sapiens.
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HORD WEELSOUG; 2003US-0459782P.
PR 3-JAN-2004; 2004US-0538246P.
XX

HORD WEELSOUG; 2004US-0538246P.
XX

HOMICAINER A J.
PA (TWREP) TREPICCHIO W L.
XX

HORD WEELSOUG; 2004US-0538246P.
XX

HOMICAINER A J.
PA (TWREP)
XX

MONITORING drug activities in vivo Profile of a gene in a peripheral broof of a gene in a peripheral broof disease and are subjected to broof sample of a patient to a refersion peripheral blood monomuclear colless to method, kit, and nucleic acid array activities in vivo. The drug is eapted in peripheral blood disease and are subjected to blood disease and are subjected to blood disease and are subjected to compart of the printed specific comparing an arget of rapamycin whimmalian target of rapamycin whimmalian target of rapamycin whimmalian target of rapamycin whimmalian target of rapamycin for mammalian target of rapamycin whimmalian target of rapamycin for mammalian target of the printed specific commat from WIPO at ftp. Wipo. Int/Pu

SA Sequence 86574 BP; 22071 A; 20398 C
Query Match
Best Local Similarity 66.7%;
Matches 16; Conservative
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The INVENTION Fracture to a purilisme interest data mission and the IMPD nucleic acid can specifically hybridise to a second cattle, and the IMPD nucleic acid can specifically hybridise to a second cattle, and the IMPD nucleic acid can specifically hybridise to a second contest acid comprising any of 15112 nucleotide sequences.

This a transformed cell having a nucleic acid comprising an IMPD nucleic acid linked to a promoter and a 3, non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and complements in the cell to cause termination of the mRNA molecule; and complementary nucleic acid sequences or its complement cell or tissue comprising a level or pattern of a molecule in a bovine cell or tissue comprising caid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the complementary nucleic acid sequences or its complementary nucleic acid sequences or the detection of the complementary nucleic acid is practicitive of the complementary nucleic acid is practicitive of the detecting the level or pattern of the complementary nucleic acid is practicitive of the complementary nucleic acid is practicity of the determining a level or pattern of the molecule. The IMPD mucleic acid is practicity or cattle constitution of constructs for use in cattle gene expression, or consider account and analysis, cattle constitution and analysis, and the construction of the constructs of preceding provine Labour in the practic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified nucleic acid molecule associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine, 88; BST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine EST associated with lactation/muscle/fat deposition #8669
   Length 86574;
                                                             Indels
76.8%; Score 19.2; DB 13; 66.7%; Pred. No. 91; ive 5; Mismatches 3;
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                                                                                                                       2 AACTUCAGGAUUCCAGAUAUGCCC 25
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11-JAN-2000; 2000US-00480902.
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                                                             16; Conservative
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(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-110599/10.
      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         ABX43504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug activity monitoring; expression profile; gene expression; peripheral blood sample; peripheral blood mononuclear cell; drug therapy; CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
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                                                                                                                                                   Gaps
                                 Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;
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0
                                                                                           6; Length 86574;
                                                                                                                                                3; Indels
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                                                                                     Score 19.2;
Pred. No. 91
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present sequence was not shown in the specification but was obtained in

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It is useful for genome mapping, gene identification and analysis, cattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                        ö
                                                                                                                                                         Length 391;
                                                                                                                                                                                                                        4; Indels
                                                                                           Sequence 391 BP; 119 A; 76 C; 99 G; 97 T; 0 U; 0 Other;
                                segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                             DB 8;
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                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                         74.4%; Score 18.6; 64.0%; Pred. No. 82;
   electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 11019; 245pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1999; 99US-0115707P
11-JAN-2000; 2000US-00480902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-110599/10.
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                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Byatt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX45854;
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(WARR/)
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX45854
XXX XXX ABX45854
XXX ABX45854
DT 21-1
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX14836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyademylated ribonucleotides to a 3' and of the mRNA molecule; and classue comprising a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 1511 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the
                                                                                                                                                                                                                              ö
breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine IMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine EST associated with lactation/muscle/fat deposition #5872.
                                                                                                                                                                                                                              ö
                                                                                                                                                                                   Score 18.6; DB 8; Length 402; Pred. No. 83;
                                                                                                                                            Sequence 402 BP; 118 A; 76 C; 105 G; 103 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Indels
                                                                             electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                5; Mismatches
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                                                                                                                                                                                                                                                                                                              339
                                                                                                                                                                                                                                                                     1 CAACUUCAGGAUUCCAGAUAUGCCC 25
                                                                                                                                                                                                                                                                                               315 CAAATTCTGGAGTCCAGATGTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                      ABX40707 standard; cDNA; 422 BP
                                                                                                                                                                                     74.48;
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                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002137139-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-JAN-1999;
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2000US-0229509P.
2000US-0229513P.
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2000US-0231968P.
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20-OCT-2000;
20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2000;
    complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid; where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and malysis, cattle breeding, preparation of constructs for use in cattle gene expression, or 15112 bovine LMFD RST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in sequence format from the USPTO web site:
                                                                                                                                                                                 ö
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41351
                                                                                                                                                                                 ö
                                                                                                                                                          Length 422;
                                                                                                                                       Sequence 422 BP; 127 A; 79 C; 112 G; 102 T; 0 U; 2 Other;
                                                                                                                                                                                Indels
                                                                                                                                                           DB 8;
                                                                                                                                                                                5; Mismatches
                                                                                                                                                           Score 18.6;
Pred. No. 83
                                                                                                                                                                                                                252 CAAATTCTGGAGTCCAGATGTGCCC 276
                                                                                                                                                                                                     1 CAACUUCAGGAUUCCAGAUAUGCCC 25
                                                                                                                                                                                                                                                                            AAK86539 standard; DNA; 609 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0186350P
2000US-019974P
2000US-0190076P
2000US-0190076P
2000US-0205515P
2000US-020467P
2000US-021515P
2000US-021515P
2000US-021647P
2000US-021647P
2000US-021647P
2000US-021647P
2000US-021647P
                                                                                                                                                         74.4%;
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2000US-0225266P.
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                                                                                                                                                                                                                                                                                                                    07-NOV-2001 (first entry)
                                                                                                                                                                    Best Local Similarity 64.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                            Query Match
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AAK86539
AC AAK86
XX
XX
XX
DT 07-NO
XX
CYCOS
XX
Human
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Human
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Human
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PD 09-AU
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PR 17-AP
PR 19-AP
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566 CAACCTCAGGACTCCAGTCATGCCC 590

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Sequence 609 BP; 152 A; 163 C; 172 G; 122 T; 0 U; 0 Other;
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08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-02496613P.
17-NOV-2000; 2000US-0249203P.
17-NOV-2000; 2000US-0249203P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000; 2000US-0251990P
                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
cutivity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
cypression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
cuplement the patients own production of (1). Additionally, (1)
cuple acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK5950 and AAM82169
represent sequences used in the exemplification of the present invention Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. Disclosure; SEQ ID NO 41351; 3071pp + Sequence Listing; English.

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74.4%; Score 18.6; DB 4; Length 609; 72.0%; Pred. No. 88;
                                           4; Indels
                                           3; Mismatches
                                                                                  1 CAACUUCAGGAUUCCAGAUAUGCCC 25
                                         18; Conservative
                     Best Local Similarity
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Gaps

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from base 1000001 (Haemophilus influenzae complete ge LOCUS AAT42063 Accession Aat42063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.6; DB 2; Length 110000; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71778 CAACTTCAGGATGCCCTTTATGCCC 71754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "myosin IXa"
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910000
1010000
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210000
310000
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243. .7889
/*tag= a
                                            f AAT42063 ;
fragments
Begin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0062858P.
97US-0062241P.
97US-0068953P.
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                                  ## Sequence split into 19 fracting Presents Name Begins Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 74.4%;
l Similarity 64.0%;
16; Conservative
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Best Local Similarity
Matches 16; Conserv
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AAT42063_16
AAT42063_17
AAT42063_18
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17-0CT-1997;
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                        AAT42063 10/c
Continuation (11
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AAX25487/c
RESULT 13
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Matches

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 1520.
                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                    1595 AACTTCAGGATTACAGATAT 1576
                                                                                                                                                                                                                                                          2 AACUUCAGGAUUCCAGAUAU 21
                                                                                                                                                                                                                                                                                                                ABL02346 standard; cDNA; 2969 BP
                                                                                                                                                                                                                           73.6%;
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                            Query Match
Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                      P-PSDB; AAY05781.
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                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2.
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Myers EW;

Li PWD,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLISTS), expressed DNA sequences (ABLISTS) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2969 BP; 881 A; 625 C; 609 G; 854 T; 0 U; 0 Other;
Claim 1; SEQ ID NO 1520; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 CAACTCGAGGATTCCATATATGC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAACUUCAGGAUUCCAGAUAUGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymucleotides, and compositions containing these polypeptides, polymucleotides, and compositions containing these polypeptides, polymucleotides, expression cassettes, transformed cells and antibodies. Conditions that can be treated by CNGC-15 and/or myosin IXa polypeptides, agonists and antagonists addationally include hearing loss, retinitis pigmentosa, obesity, hypogonadism, sterility, polydactyly, brachydactyly, syndactyly, mental retardation, renal abnormalities, hypertension, diabetes and cardiovascular abnormalities (all claimed). Methods for the expression and detection of CNGC-15 and myosin IXa nucleotides and polypeptides are also provided
                                                                                                                                                                                                                                                                                                                                                                          nucleotide sequence comprising the present sequence, or nucleotides 243-7085, 243-680, 683-2399, 959-977, 2404-2747, 3158-3740 or 6473-6899, is claimed. The cDNA was isolated from a human BAC contig that spanned chromosomal region 15p22-23; the Bardet-Biedl syndrome gene maps to this locus. Myosin IXa is thus useful in the study, diagnosis and therapy of Bardet-Biedl syndrome and Usher syndrome. The invention discloses myosin IXa and cyclic nucleotide gated channel-15 (CMCC-15) polypeptides,
                                                                                                                                                                                                                                                                                                                                              is the nucleotide sequence of human myosin IXa cDNA. An isolated
                                                                                                                                                                                     Myosin IXa and cyclic nucleotide gated channel-15 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8473 BP; 2703 A; 1736 C; 1891 G; 2143 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Claim 11; Fig 2; 69pp; English.
                                                                        WPI; 1999-277643/23.
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Search completed: July 30, 2005, 12:18:08
Job time : 311.446 secs
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Gaps

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1; Indels

Length 8473;

Score 18.4; DB 2; Pred. No. 1.6e+02; 6; Mismatches

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Gaps

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3; Indels

5; Mismatches

Score 18.2; DB 4; Length 2969; Pred. No. 1.7e+02;

72.8%;

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July 30, 2005, 11:50:11 ; Search time 2561.15 Seconds (without alignments) 371.555 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                 68479088
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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25
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9b est6: *

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No. Score Match Length DB ID Description	Result		* Ouery			SUMMAKIES		
1 25 100.0 388 1 AA100508 AA100508 AA100508 AA100508 AA100508 AA100508 AA100508 AA100508 BF694585 6020814 3 2 34 93.6 823 2 BF694585 BF69989 BF69989 BF69989 BF69989 BF69989 BF629985 BF6279965 CC573906 CC573906 <td>No.</td> <td>Score</td> <td></td> <td>Length</td> <td>DB</td> <td><u>a</u> :</td> <td>Descripti</td> <td>no</td>	No.	Score		Length	DB	<u>a</u> :	Descripti	no
2 23.4 93.6 823 2 BF694585 602014 3 23.4 93.6 92.5 2 BF789989 BF729985 BF729985 GC247996 4 21.8 87.2 370 9 CG573906 CG573913111 CG553907 CG533907 CG532939 CG550907 CG553907 CG553907 CG553907 </td <td>0</td> <td>25</td> <td>100.0</td> <td>388</td> <td>7</td> <td>AA100508</td> <td>AA100508</td> <td>zn51c07.r</td>	0	25	100.0	388	7	AA100508	AA100508	zn51c07.r
3 23.4 93.6 925 2 BF789989 BB789989 B022499 4 21.8 87.2 370 9 CG573906 CG573907 CG573907 CG573907 CG573907 CG573907 CG573907 CG570757 BF693401 CG501751 BF693707 BF693707 BF693707 BF693707 BF793708 BF7937270 BF7937270 BF7937270 BF	c 0	23.4	93.6	823	~	BF694585	BF694585	602081409
4 21.8 87.2 216 2 BF229965 CCS53967 CGS73966 OST2061 5 21.8 87.2 370 9 CG533907 CG573966 CG57396 CG57396 CG57396 CG57396 CG57396 CG57396 CG572061 GG572061 GG57396 CG57396 CG57396 CG57396 CG57396 CG57396 CG57396 CG57396 CG572061 GC57396 CG57396	c o	23.4	93.6	925	~	BF789989	BF789989	602249960
5 21.8 87.2 370 9 CG573906 CG573906 CG573907 CG5731 CG5737 CG57404 CG57400 CG57400 CG57400	4	21.8	87.2	216	N	BF229985	BF229985	MR2-CT045
6 21.8 87.2 380 9 CG539807 CG50757 ERF03761 ERF070751 CG020757	C S	21.8	87.2	370	0	CG573906	CG573906	OST206109
7 21.8 87.2 601 2 BF570751 BEF770751 6020757 8 21.8 87.2 73 2 BF6683401 BF66859401 6020810 9 21.8 87.2 73 2 BF668530 BT50810	9	21.8	87.2	380	φ	CG539807	CG539807	OST131162
8 21.8 87.2 739 2 BF693401 BF693401 BF693401 6020910 9 21.8 87.2 48.3 4 BI668593 AIZ25530 AIZ25530 AIZ35393 6032939 10 20.8 83.2 51.5 8 AZ513867 AZ513867 AZ513867 IM0360J 12 20.8 83.2 673 1 AV726731	7	21.8	87.2	601	~	BF570751	BF570751	602075762
9 21.8 87.2 863 4 BI668533 BI668593 6032339 10 20.8 83.2 51.5 8 AZ513867 AZ51387 AZ513387 AZ51387	ص ص	21.8	87.2	739	~	BF693401	BF693401	602081037
10 20.8 83.2 43.2 1 AI225530 AI225530 AI225530 uj05b10 11 20.8 83.2 515 8 AZ513867 AZ5513867 AZ551376 AZ551		21.8		863	4	BI668593	BI668593	603293903
11 20.8 83.2 515 8 AZ513867 AZ513867 AZ513867 AZ513867 AZ513867 AZ513867 MAZ513867 MAZ513867 MAZ513867 MAZ513867 MAZ5131 AV726731 AV7267332 AV7267332	c 10	20.8	83.2	432	7	AI225530	AI225530	uj05b10.y
12 20.8 83.2 673 1 AV726731 AV726732 AV72772 AV72732 <	-	20.8	83.2	515	ထ	AZ513867	AZ513867	1M0360J08
13 20.8 83.2 698 2 BF791086 BF791086 6022511 14 20.2 80.8 473 1 AA193133 AA193133 AA193133 AA193133 AA193133 2013003 15 20.2 80.8 687 4 BG427535 BG427535 6024645 17 20.2 80.8 687 6 CA163435 CA163436 BG72667		20.8	83.2	673	H	AV726731	AV726731	AV726731
14 20.2 80.8 473 1 AA193133 AA193133 Zq13c03 15 20.2 80.8 587 2 BF687772 BF687772 6020668 16 20.2 80.8 657 4 BG427535 GA163435 CA163435 CA163436 CA163435 CA163436 CA163436 <td>•</td> <td>20.8</td> <td>83.2</td> <td>698</td> <td>7</td> <td>BF791086</td> <td>BF791086</td> <td>602251165</td>	•	20.8	83.2	698	7	BF791086	BF791086	602251165
15 20.2 80.8 587 2 BF687772 6020668 16 20.2 80.8 687 4 BG427535 BG427535 6024945 17 20.2 80.8 687 6 AG427535 CAL63435 SCRLR231 18 20.2 80.8 757 2 BF791087		20.2	80.8	473	-	AA193133	AA193133	zq13c03.r
16 20.2 80.8 657 4 BG427535 BG427535 6024945 17 20.2 80.8 687 6 CA163435 CA163435 CA163435 CCA163435 CCA162436 CA1645667 GCA16457 GCA16457 CCA162436 CCA16240 CCA16240 CCA16240 CCA16240 CCA16240 C		20.2	80.8	587	7	BF687772	BF687772	602066821
17 20.2 80.8 687 6 CA163435 CA163435 CA163435 CAL63435 SCRLKZ3 18 20.2 80.8 757 2 BF791087 BG72667 BG72667 BG42667 BG42667 BG426667 BG426667 BG426667 BG426667 BG426667 BF672700 6021520 21 19.2 76.8 314 2 BB45938 BE645938 232575 22 19.2 76.8 317 7 CNZ53955 CNZ53955 BIP0017 23 19.2 76.8 414 2 AW066689 AW066689 683006E		20.2	80.8	657	4	BG427535	BG427535	602494560
18 20.2 80.8 757 2 BF791087 BF791087 602511 19 20.2 80.8 845 4 BG426667 BG426667 BG426667 6024932 20 20.2 80.8 845 2 BF672700 6021520 21 19.2 76.8 314 2 BB845938 BE845938 232575 22 19.2 76.8 317 7 CNZ53955 CNZ53955 BF0017 23 19.2 76.8 414 2 AN066689 AN066689 <td></td> <td>20.2</td> <td>80.8</td> <td>687</td> <td>9</td> <td>CA163435</td> <td>CA163435</td> <td>SCRLRZ311</td>		20.2	80.8	687	9	CA163435	CA163435	SCRLRZ311
19 20.2 80.8 826 4 BG426667 BG426667 6024932 20 20.2 80.8 845 2 BF672700 6021520 21 19.2 76.8 314 2 BE845938 BE845938 BE845938 232575 22 19.2 76.8 317 7 CM253955 CM253955 BIP0017 23 19.2 76.8 342 6 CD706840 CD706840 CD706840 CB70689 683106E 24 19.2 76.8 414 2 AW066689 683106E		20.2	80.8	757	N	BF791087	BF791087	602251166
20 20.2 80.8 845 2 BF672700 6021520 21 19.2 76.8 314 2 BE845938 BE845938 BE845938 232575 22 19.2 76.8 317 7 CNS53955 CNS53955 BL90017 23 19.2 76.8 342 6 CD706840 CD706840 CD706840 CD706840 SST2338 24 19.2 76.8 414 2 AW066689 AW066689 AW066689 683006E	Н	20.2	80.8	826	4	BG426667	BG426667	602493208
21 19.2 76.8 314 2 BE845938 BE645938 232575 22 19.2 76.8 317 7 CNZ53955 CNZ53955 BIP0017 23 19.2 76.8 347 7 CNZ53955 CD706840 CD706840 24 19.2 76.8 414 2 AW066689 683006E	7	20.2	80.8	845	8	BF672700	BF672700	602152006
22 19.2 76.8 317 7 CN253955 . CN253955 23 19.2 76.8 342 6 CD706840 CD706840 24 19.2 76.8 414 2 AW066689 AW066689	7	19.2	76.8	314	~	BE845938	BE845938	
23 19.2 76.8 342 6 CD706840 CD706840 24 19.2 76.8 414 2 AW066689 AW066689	7	19.2	76.8	317	7	CN253955	CN253955	BIP0017 B
76.8 414 2 AW066689 AW066689	~	19.2	76.8	342	9	CD706840	CD706840	EST23367
	24	19.2	76.8	414	7	AW066689	AW066689	683006E11

AQ633324 RPCI-11-4	BG349404 947030B11	CK944021 4068070 B	BG349720 947030B11	CB455616 712772 MA	CK979258 4111048 B	BG866086 602784901	CE807695 tigr-gss-	BF681266 602155541	BF790177 602249479	AW642399 cm18c11.w	AQ321144 RPCI11-10	BY734522 BY734522	AL508468 AL508468	CR465805 CR465805	CB708790 AMGNNUC:S	AA892501 EST196304	BE328934 hg32d07.x	BF416636 UI-R-CAO-	AI717137 UI-R-Y0-a	BI541804 455662 MA
AQ633324	BG349404	CK944021	BG349720	CB455616	CK979258	BG866086	CE807695	BF681266	BF790177	AW642399	AQ321144	BY734522	AL508468	CR465805	CB708790	AA892501	BE328934	BF416636	AI717137	BI541804
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76.	76.	76.	76.	76.	76.	76.	76.	76.	76.	75.	75.	75.	75.2	74.	74.	74.	74.	74.	74.	74.
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19	19	13	13	13	13	19	13	13	13	18	18	18	18	18	18	18	18	18	18	18
25	c 26	c 27	c 28	c 59	30	c 31	c 32	33	c 34	c 35	36	37	38	39	40	c 41	. c 42	c 43	C 44	45

ALIGNMENTS

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SOURCE
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                                         RESULT 3
BF789989/c
                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                        ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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/lab_host="hHAGE:4245770"
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/clone=lib="NHH MGC 81"
/note="organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil
(Glontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil
(Glontech); Site 3: and 3' adaptors were used in cloning as follows: S' adaptor sequence: S'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: S'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: S'-ATTCTAGAGGCCGACATATGGCC-3'
and 3' adaptor sequence: S'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: S'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: S'-CACGGCCATTATGGCC-3'
and S'-CATTCTAGAGGCCGACATATGGCC-3'
and S'-CATTCTAGAGCCCGACATATGGCC-3'
and S'-CATTCTAGAGCCCGACATATGGCC-3'
and S'-CATTCTAGAGCCCGACATATGGCC-3'
and S'-CATTCTAGGGCCGACATATGGCC-3'
and S'-CATTCTAGGGCCGCACATATGGCC-3'
and S'-CATTCTAGGCC-3'
and S'-CATTCTAGGC
/note="Organ: skeletal muscle; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATICGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTITITITITITITITITI 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF694585 82-DEC-2000 602081409F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245770 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 823)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLCM1060 row: a column: 03
High quality sequence stop: 571.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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llarity 72.0%; Pred. No. 6.6;
Conservative 6; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                         DB 1; Length 388;
                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                              100.0%; bcc. 76.0%; Pred. No. 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                  BF694585.1 GI:11979993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/155 colonies conteained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
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1 (bases 1 to 216)
Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
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BF789989 92249960F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4328127 5',
                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1817 row: h column: 16
High quality sequence stop: 527.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        TH. MGC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tysuve Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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BF229985.1 GI:11167490
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                                                                                                                                                                    Homo sapiens (human)
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                                                         mRNA sequence.
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AUTHORS
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Query Match 87.2
Best Local Similarity 68.0
Matches 17; Conservative
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CG539807/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/dow_stage="Adult"
/dow_stage="Adult"
/clone_lib="CT0456"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,P., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=MR2-CT0456-220 900-004-e07&t3=2000-09-22&t4=1)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 370)
                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Best Local Similarity 72.0%; Pred. No. 28;
Matches 18; Conservative 5; Mismatches
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High quality sequence start: 19
High quality sequence stop: 215.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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El (Dases I 
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Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
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/clone_lib="Mus musculus 129Sv/Ev"
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clone_lib="Mus musculus 129Sv/Ev"
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87.2%; Score 21.8; D
Best Local Similarity 68.0%; Pred. No. 32;
Matches 17; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
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/clone="OST206109"
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                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG539807.1 GI:37326379
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/clone=ITMAGES1424584"
/lab_host=ITMAGES14."
/lab_host=ITMAGCS11."
/clone lib="NHH MGC 81"
/clone lib="NHH MGC 81"
/note="Organ: muscle [ skeletal ]; Vector: pDNR-LIB
(Clontech); Site_1: Sfil (ggccgctctggcc); Site_2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: S' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGCGCACATG-dT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clone and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 863)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshhyuki and Piero Carninoi (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://mage.llnl.gov

Plate: LLAM11793 row: f column: 01
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                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1059 row: i column: 09
High quality sequence stop: 729.
High quality sequence stop: 729.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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BI668593.1 GI:15582826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.2%;
Best Local Similarity 68.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alto, CA)."
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                                       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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/db_xref="taxon:966"
/db_xref="taxon:966"
/clone="IMAGE:42429"
/tissue_type="melanotic melanoma, high MDR"
/tissue_type="melanotic melanoma, high MDR"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 62"
/clone lib="NIH MGC 63"
/clone lib="NIH MGC 62"
/clone lib="NIH MGC 63"
/clone lib="NIH MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.

E. 1 (bases 1 to 601)

E. 1 (bases 1 to 601)

I. Unpublished (1999)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM1052 row: 1 column: 15

High quality sequence stops: 598.
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                                                                                                                                                                                                              BF570751 601 bp mRNA linear EST 12-DEC-2000 602075762F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4242974 5',
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
   390 CAACTICCAGAITCCAGAIAIGCCC 366
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                                                                                                                                                                                                                                                                                        nRNA sequence.
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Best Local Similarity
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BF693401/c
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Gaps

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Indels

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/clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pWE185-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTATGG], digested
and cloned into distinct DraIII sites of the pWE185-FL3
vector (5; site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 05-OCT-2000
                                                                                                                                                                                                                                                        performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 515)
Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ513867
1M0360J08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0360J08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
12, USA
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/clome lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                83.2%; Score 20.8; DB 1; Length 432;
64.0%; Pred. No. 95;
ive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: J column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
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Seg primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 CANCTTCAGAATTCCAAATATGCCC 357
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/clone="UUGC1M0360J08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAACUUCAGGAUUCCAGAUAUGCCC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Best Local Similarity
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AZ513867/c
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                                                                                                                                                                                                                           /clone_lb="MINUM MGC 96"
/clone_logan: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_l: BamH! Site_2: Sall-XhoI pBluescript KS+); Site_l: BamH! Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMM/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:975327
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.8; DB 4; Length 863; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                 /mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5313024"
/tissue type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 37;
6; Mismatches
                                                                           /organism="Homo sapiens"
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The WashU-HHMI Mouse EST Project
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High quality sequence stop: 425.
Location/Qualifiers
High quality sequence stop: 689
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                             Location/Qualifiers
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/strain="C57BL"
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGR=1438353"
/lab host="MHAGC 81"
/clone=lib="NHH MGC 81"
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/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note=chorgan: muscle (skeletal); Vector: pDNR-LIB
/note=ch); Site 1: $fil (ggccgctcggcc); Site 2: $fil
(Glontech); Site 1: $fil (ggccgctcggcc); Site 2: $fil
(Glontech); Site 2: $fil (spccgctcggcc); Site 2: $fil
(Glontech); Site 2: $fil (spccgcccggcc); Site 2: $fil
(Glontech); Site 2: $fil
                                                                                                                                                                         BF791086 698 bp mRNA linear EST 12-JAN-2001
602251165F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338353 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1214 row: b column: 18
High quality sequence stop: 162.
Location/Qualifiers
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Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota: Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
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zq13c03.rl Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:629572 5' similar to TR:G307311 G307311 HISTONE H4. ;, mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Homo sapiens
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BF791086/c
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: pBluescript sk(-); Site_l: EcoRI; Site_2:
Xhol"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.8; DB 1; Length 673; Pred. No. 1e+02; 6; Mismatches 2; Indels
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/dev_stage="Adult"
/lab_host="SOLR"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTCBNF02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| :||||| :||||| 514 AACATCAGGATTCCAGGTATGCCC 491
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Best Local Similarity
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AV726731/c
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Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., More, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Waterston, R. and Wilson, R. Washu-NCI human EST Project

L. Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notes Torgan: skeletal muscle; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF687772 587 bp mRNA linear BST 22-DEC-2000 602066821F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065893 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM902 row: j column: 06
High quality sequence stop: 585.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:629572"
/tissue_type="muscle"
/dev stage="adult"
/lab_nost="SOLR (kanamycin_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Stratagene muscle 937209"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 80.8%; Score 20.2; DB 1; 1 Similarity 68.0%; Pred. No. 1.9e+02; 17; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5049806"
/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 CAACTTCAGATTCCCAGATATGCCC 327
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BF687772
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/Lissue type="glioblastoma" //Lissue type="glioblastoma" / Lissue type="glioblastoma" / Lisu host="PHRIOB (TI phage-resistant)" / Lisu host="Billioblastom" 
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68.0%; Pred. No. 1.9e+02;
tive 5; Mismatches 3;
organism="Homo sapiens"
                                                                                                                                                                                               clone="IMAGE:4065893"
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                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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TYPE: DNA
ORGANISM: Human
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Sequence 1, Appli
Sequence 2, Appli
Sequence 16009, A
Sequence 1533, A
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Sequence 11820, A
Sequence 17182, A
Sequence 49, Appli
Sequence 14944, A
Sequence 14946, A
Sequence 14946, A
Sequence 16911, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 16918, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44986, A
Sequence 44987, A
Sequence 44988, A
Sequence 13032, A
Sequence 16101, A
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Sequence 16930, A
Sequence 16931, A
Sequence 14340, A
                                                                                         (without alignments)
453.500 Million cell updates/sec
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                                                                            July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
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(cgn2_6/ptodata//ina/5A_COMB.seq:*

(cgn2_6/ptodata//ina/5B_COMB.seq:*

(cgn2_6/ptodata//ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/ROTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
version 5.1.6
- 2005 Compugen Ltd.
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US-09-949-016-44988
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US-09-949-016-16101
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US-09-949-016-16930
US-09-949-016-16930
US-09-949-016-16931
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          1202784 seqs, 818138359 residues
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Maximum Match 1008
Listing first 45 summaries
                                                     - nucleic search, using sw model
                                                                                                                                                                                  IDENTITY NUC Gapop 10.0 , Gapext 1.0
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 44986
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 2009-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
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Sequence 182464,
Sequence 182582,
Sequence 182583,
Sequence 29747, A
Sequence 13725, A
       14344, A
14344, A
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US-09-949-016-14344
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US-09-949-016-14347
US-09-949-016-1296
US-09-949-016-12465
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Patent No. 6812339
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Matches 16; Conserv
       RESULT 2
US-09-949-016-44987/c
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ZIP: 20850
COMPUTER READABLE FORM:
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US-09-949-016-16101/c
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ORGANISM: Human
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US-09-949-016-13032/c

JUS-09-949-016-13032, Application US/09949016

Sequence No. 6812339

GENERAL INCORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-1
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAESEQ for Windows Version 4.0

LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                         Length 601;
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44987
LENGTH: 601
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; Sequence 4498, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; ORGANISM: Human
US-09-949-016-44988
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                      US-09-949-016-44987
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Sequence 16101, Application US/09949016

Sequence 16101, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-14-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16101

LENGTH: 237241

LENGTH: 237241
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TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                      Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.2%; Score 18.8; I
Best Local Similarity 63.6%; Pred. No. 43;
Matches 14; Conservative 6; Mismatches
                                                                                                                                                                       Score 19.2; 1
Pred. No. 26;
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CITY: Rockville
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                      2 AACTUCAGGAUUCCAGAUAUGCCC 25
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) ORGANISM: Human
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(165651)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature; LCCATION: (1)...(237241); CTHER INFORMATION: n = A,T,C or G US-09-949-016-16101
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Best Local Similarity 66.7%;
Matches 16; Conservative
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DB 4;
                             : PB186P1C1
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64.0%; Pred. No. 74;
tive 5; Mismatches
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                                                                                                                                                       ;
TTPE: nucleic acid
;
STRANDEDNESS: double
;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
                    REPERENCE/DOCKET NUMBER: PB18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
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      REGISTRATION NUMBER: 40,302
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1595 AACTTCAGGATTACAGATAT 1576
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Best Local Similarity 64.0
Matches 16; Conservative
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US-09-172-422-2
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Best Local Similarity
Matches 13; Conservé
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Hamilton O. Smith
J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1830121;
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ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20850
COMPUTER READAILE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFTCATION: «Unknown>
PRIOR APPLICATION ON THE CONTROL OF TILING DATE: 1995-06-07
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIPICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4%; Score 18.6; I
64.0%; Pred. No. 74;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1071778 CAACTTCAGGATGCCCTTTATGCCC 1071754
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marke
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAACUUCAGGAUUCCAGAUAUGCCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert D. Fleischmann
Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kenley K. Hoover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 64.0
Matches 16; Conservative
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US-09-643-990A-1/c
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Sequence 16009, Application US/09949016

Batent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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APPLICANT: Adams, Arwen E.
APPLICANT: Chiu, Choi Ying
APPLICANT: Chiu, Choi Ying
APPLICANT: Corman, Susan W.
APPLICANT: Gorman, Song
APPLICANT: Leng, Song
APPLICANT: Sheffield, Val
APPLICANT: Sheffield, Val
APPLICANT: Welch, Juliec
TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, PITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
FILE REFERENCE: 200130.442
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FRREEGG for Windows Version 3.0
SEQ ID NO 2
LENGTH: 8473
                                                          Gaps
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Length 1830121;
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                                                          4; Indels
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TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-783-1
       LENGTH: 15572
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FACELL S. J. Craig et al.
FILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.
FILLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 17533
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                                                                                                                                                                                                                                               69.6%; Score 17.4; DB 4; Length 66247; 68.4%; Pred. No. 1.7e+02; tive 5; Mismatches 1; Indels 0;
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US-09-424-783-1/c

Sequence 1, Application US/09424783

SEQUENCE 1, INFORMATION:

APPLICANT: Histimura, Sedichiro

APPLICANT: Histimura, Sedichiro

APPLICANT: Barsoumian, Edward Leon

TITLE OF INVENTION: Human Type 3 Ryanodine Receptor

TITLE OF INVENTION: and DNA Molecules Coding Therefor

TITLE OF INVENTION: Human Type 3 Ryanodine Receptor

CURRENT APPLICATION NUMBER: US/09/424,783

CURRENT PILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 1
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16009
LENGTH: 66247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17533, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 68.43
Matches 13; Conservative
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Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-949-016-17533/c
                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                  US-09-949-016-16009
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ESCULT 1820

| Sequence 11820, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REPERENCE: CL0001307
| CURRENT PILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR PAPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PILING DATE: 2000-10-20
| PRIOR PILING DATE: 2000-09-08
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENTH: 192700
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                                       Gaps
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Query Match 68.8%; Score 17.2; DB 4; Length 15572; Best Local Similarity 63.6%; Pred. No. 1.6e+02; Matches 14; Conservative 5; Mismatches 3; Indels 0;
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                                                                                                     13920 CAACTCCAAGCTTCCAGATAIG 13899
                                                                              1 CAACUUCAGAUUCCAGAUAUG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAACUUCAGGAUUCCAGAUAUG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-17182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-17182
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Sequence 3, Application US/09734675

Barent No. 6365391

GENERAL INFORMATION:
APPLICANT: WESSTER, Marion et al
TITLE OF INVENTION: LOSLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C1000862
CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 38844
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                                                                                                                  EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 897
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER APPLICATION NUMBER: 60/048, 877
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-12-18
EARLIER FILLING DATE: 1997-12-18
EARLIER FILLING DATE: 1997-12-18
EARLIER FILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1997-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (570)
; OTHER INFORMATION: n equals a,t,g, or
US-09-205-258-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-734-675-3
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                                                                    Gaps
      Length 192704;
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                                                                    3; Indels
ch 68.8%; Score 17.2; DB 4; Similarity 63.6%; Pred. No. 2.5e+02; 14; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
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EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/049,020
APPLICATION NUMBER: 60/048,876
PILLING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,892
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,915
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,019
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,019
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85389 CCATTTCAGGAATCCAGATATG 85410
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APPLICATION NUMBER: 60/048,916
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
                                                                                                                           1 CAACUUCAGGAUUCCAGAUAUG 22
                                                                                                                                                                                                                                                                                 RESULT 14
US-09-205-258-49/c
'Sequence 49, Application US/09205258
'Patent No. 6555174
'GENERAL INFORMATION:
   Query Match
Best Local Similarity
                                                                    Matches
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0; Gaps 5; Indels Matches 16; Conservative 4; Mismatches

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Search completed: July 30, 2005, 15:05:43 Job time : 98.2027 secs

Primer fo Homo sapi

Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Secreted Homo sapi Sequence Homo sapi

Homo sapi Homo sapi Secreted

sapi sapi sapi

Ношо

score:

Sequence:

OM nucleic

on:

Run

Scoring table:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AK129806

AF132048

AF132048

BD127437

BD127436

AK075339

AK075339

AK102276

AY102276

AY102276

AY102277

AY102278

AX102273

AX102273
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Liew, C.C., Marshall, W.E. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 33274 12-SEP-2002;
Chondrogene Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 24; DB 6; Length 144;
Pred. No. 3.6;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 bp DNA Sequence 33274 from Patent W002070737. CQ688348.1 GI:42220578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQ712889 170 bp DNJ
Sequence 57815 from Patent WO02070737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                     AB020693
AY123250
AY123249
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AY102276
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AF148538
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AF333336
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CQ712889.1 GI:42273746
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Best Local Similarity 79.2%; I
Matches 19; Conservative 5;
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DEFINITION
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CQ688348/c
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CQ712889/c
LOCUS
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CQ68336 Sequence
GG514 human STS W
CQ702205 Sequence
AX895341 Sequence
AX895341 Sequence
BD030874 Sequence
CQ781164 Sequence
CQ781164 Sequence
BD127677 Primer fo
CQ78338 Sequence
BD127047 Primer fo
BC07109 Homo sapi
AX172726 Homo sapi
AX172726 Homo sapi
AX172726 Homo sapi
BD194907 86 human
CQ855235 Sequence
BC071848 Homo sapi
BD211848 Homo sapi
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Primer fo
Homo sapi
Homo sapi
                                                                                             July 30, 2005, 11:00:21; Search time 702.486 Seconds (without alignments) 1655.441 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQ688348 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                   9416466
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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CQ709205
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CQ709205
CQ786446
AX895341
BD030874
CQ781164
BD127047
BC072338
BD127047
BC07109
BC07109
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BC071848
BD231889
AF087901
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Maximum DB seq length: 200000000
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9b ow: *
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9b pb: *
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PAT 03-FEB-2004

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Result

PAT 03-FEB-2004

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

ORIGIN

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1. .207

Organism="Homo sapiens"

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="743_G4; 758_B5; 919_A_6; 919_F_3; 909_E_11; 222.4
cR from top of Chr2 Iinkage group"
2. .176
2. .21
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prepared with primer pairs derived from Z38593 -- dbEST.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 24; DB 11; Length 207;
Best Local Similarity 79.2%; Pred. No. 3.3;
Matches 19; Conservative 5; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liew, C.C., Marshall, W.E. and Zhang, H. Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 54131 12-SEP-2002; Chondrogene Inc. (CA)
Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900 Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQ709205 370 bp DNA Sequence 54131 from Patent W002070737.
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1.370
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                           dNTPs: each 4 nm
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul
                                                                                  Email: thudson@genome.wi.mit.edu
                                                                                                                        Primer A: TAGCTCCACCATCTCTGCAA
Primer B: GTCTTGACTGCCATGTGTTCA
STS size: 175
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (156. .176)
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Polymerization:
PCR Cycles: 35
Thermal Cycler:
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MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
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Primer: each 5 p
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 207)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Score 24; DB 6; Length 170;
Best Local Similarity 79.2%; Pred. No. 3.5;
Matches 19; Conservative 5; Mismatches 0; Indels
                                            Liew, C.C., Marshall, W.E. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02010737-A 57815 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 28762 12-SBP-2002;
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Whitehead Institute/MIT Center for Genome Research
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605614
605614.1 GI:858859
STS; STS sequence; primer; sequence tagged site.
Homo sapiens (human)
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Sequence 28762 from Patent WO02070737.
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100.0%; Score 24; DB Best Local Similarity 79.2%; Pred. No. 3.4; Matches 19; Conservative 5; Mismatches
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|mol_type="unassigned DNA"
|db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Location/Qualifiers
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source

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SOURCE

ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS TITLE

JOURNAL FEATURES

CQ683836/c DEFINITION

RESULT 3

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PAT 03-FEB-2004

linear

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS TITLE

JOURNAL COMMENT

PAT 27-AUG-2002

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C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                 C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 496)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Sequence tag and encoded human protein
Patent: JP 2001269182-A 7120 02-OCT-2001;
                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 2001269182-A/7120
02-007-2001
24-FEB-1000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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                                          linear
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                                 Sequence tag and encoded human protein.
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100.0%; Score 24; DB
Best Local Similarity 79.2%; Pred. No. 2.8;
Matches 19; Conservative 5; Mismatches
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/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                        BD030874.1 GI:22572616
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                                                                                                      JP 2001269182-A/7120.
Homo sapiens (human)
Homo sapiens
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     RESULT 8
BD030874/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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; Score 24; DB 6; Length 370;
Pred. No. 3;
5; Mismatches 0; Indels
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    .496
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AX895341.1 GI:40050225
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Best Local Similarity 79.2%; I
Matches 19; Conservative 5;
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Homo sapiens
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AX895341/c
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ö PAT 17-MAR-2004 Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Primers for synthesizing full length cDNA clones and their use Patent: BP 1396543-A 1304 10-MAR-2004; Research Association for Biotechnology (JP) Location/Qualifiers ; 0 100.0%; Score 24; DB 6; Length 536; 79.2%; Pred. No. 2.8; linear Query Match Best Local Similarity

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PRI 29-JUN-2004
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Primer for synthesizing full-length cDNA and use thereof.
BD127047
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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JP 2002017375-A/2478.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 559)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 2478 10-MAR-2004; Research Association for Blotechnology (JP) Location/Qualifiers
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SHINICHI KOJIWA,
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Best Local Similarity 79.2%; Pred. No. 2.7;
Matches 19; Conservative 5; Mismatches ۱۰ تسکیا
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Pred. No. 2.7;
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    .559
    /organism="Homo sapiens"
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/mol_type="genomic DNA"
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JP 2002017375-A/2478
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Best Local Similarity 79.2%;
Matches 19; Conservative 5
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JP 2002017375-A/1304
22-JAN-2002
07-JUL-2000
JP 200253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Patent: JP 2002017375-A 1304 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Pred. No. 2.8;
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/organism="Homo sapiens"
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                                                                        76 ATTCCACCAGTGCCTCAGATAGGA 99
                                                  1 AUUCCACCAGUGCCUCAGAUAGGA 24
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                                                                                                                                                                                                                                          3D125873.1 GI:23220818
                                                                                                                                                                                                                                                            JP 2002017375-A/1304.
Homo sapiens (human)
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Homo sapiens
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Matches 19; Conservative
              Conservative
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              19;
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CQ782338
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                Matches
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PRI 11-MAY-2004

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/db_xref="LocusID:57142"

/db_xref="MIM:604475"

112. 711

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); CDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (20-APR-2004) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba
292-0818, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975,
Pax:81-438-52-3986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens cDNA PSEC0023 fis, clone: NT2RP1000386. AK172726 AK172726.1 GI:47115505 Oligo capping; fis (full insert sequence). Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 9; Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 9; Length 1206; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                          IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.4;
5; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             976 ATTCCACCAGTGCCTCAGATAGGA 953
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cell_type="tera"
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Best Local Similarity 79.2%; I
Matches 19; Conservative 5;
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AK172726/c
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                                                                  CDS
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1. (bases 1 to 1079)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.P., Zeeberg, B. Buetow, K.H., Schaner, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Schaefer, C.F., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Frange, C., Kaha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Mullahy, S.J., Boack, S.A., McKernan, P.J., McKernan, K.J., Mullahy, S.J., Boack, S.A., McRands, S.W., Villalon, D.K., Walze, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Yillalon, D.K., Walze, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Baukesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimocod, J., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissaue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAL Plate: 21 Row: h Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"
   lomo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone MAGE:4291127), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue type="Skeletal Muscle"
/clone lib="NIH MGC_81"
/lab_host="DH10B"
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                                                            BC007109
BC007109.1 GI:13937989
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                                                                                                                                              Homo sapiens (human)
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trausberg, R.
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PI ANN M FERRIE, GUO LIANG YU, JIAN NI, PING FENG
PC CO7H21/02, CO7H21/04, C12N5/00, C12N5/04, C12N5/10 PC
,C12N5/16, C12N15/04, C12N15/00, C12N5/11, C12N15/12, C12P21/04, C12P21/06 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC 86 human secreted proteins
FF Key
Location/Qualifiers
FF Rey
Location/Qualifiers
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Olsen, H.S., Shi, Y., Rosen, C.A., Ruben, S.M., Lafleur, D.W.,

Olsen, H.S., Ebher, R.

Ebher, M. Yun, G.L., Ni, J. and Feng, P., Greene, J.M.,

Ferrie, A.M., Yun, G.L., Ni, J. and Feng, P., Greene, J.M.,

Ferrie, A.M., Yun, G.L., Ni, J. and Feng, P., Greene, J.M.,

B6 human secreted proteins

L Patcent: JP 200214090-A 78 14-MAY-2002;

HUMAN GENOWE SCIENCES INC

OS Unidentified

PD 14-MAY-2002

PF 11-JUN-1997 US 60/049549, 13-JUN-1997 US 60/049508 PR

13-JUN-1997 US 60/049569, 13-JUN-1997 US 60/049608 PR

13-JUN-1997 US 60/049609, 13-JUN-1997 US 60/049610 PR

13-JUN-1997 US 60/049609, 13-JUN-1997 US 60/05091 PR

13-JUN-1997 US 60/04961, 13-JUN-1997 US 60/05911 PR

13-JUN-1997 US 60/04961, 13-JUN-1997 US 60/05865 PR

13-JUN-1997 US 60/052884, 12-SEP-1997 US 60/05865 PR

12-SEP-1997 US 60/058863, 12-SEP-1997 US 60/05865 PR

12-SEP-1997 US 60/058872, 12-SEP-1997 US 60/06881 PR

12-SEP-1997 US 60/068872, 12-SEP-1997 US 60/06885 PR

12-SEP-1997 US 60/068872, 12-SEP-1997 US 60/06885 PR

12-SEP-1997 US 60/068872, 02-OCT-1997 US 60/06885 PR

12-SEP-1997 US 60/06084, 02-OCT-1997 US 60/06085 PR

13-ELEUR,

PI HERRIE, SULSEN, REINHARD EBNER, LAURIE A BREMER, PAUL YOUNG, PR

PI HERRIE, COTHILLOR, COTHILOR, CILNE/UC, CILNE/UC, COTHILOR, CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Score 24; DB 6; Length 1213;
Best Local Similarity 79.2%; Pred. No. 2.4;
Matches 19; Conservative 5; Mismatches 0; Indels 0
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                                                                                                                                                                                       DNA
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Search completed: July 30, 2005, 12:54:29
Job time : 703.486 secs
                                                                                                                                                                                                                86 human secreted proteins.
BD194907
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JP 2002514090-A/78.
                                                                                                                                                                                                                                                                                                                                          unidentified
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                                                                                                                               RESULT 15
BD194907/c
                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

July 30, 2005, 10:32:26; Search time 296.108 Seconds (without alignments) 479.804 Million cell updates/sec

US-09-544-776-5 24 Title:

Perfect score:

1 auuccaccagugccucagauagga 24 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* 1: qeneseqn1980s:* geneseqn1980s:* Database

geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003ds:* geneseqn2003cs:* geneseqn2004as:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2003as:* geneseqn2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2004bs:*

SUMMARIES

		•				
Result		Query				
No.	Φ	Match	Match Length DB	DB	ΩI	Descripti
-	24	100.0	24	į m	AAC64409	Aac64409
0	24	100.0	496	· ~	AAC07129	Aac07129
က	24	100.0	536	4	AAK92844	Aak92844
4	24	100.0	536		ADL29271	Ad129271
S	24	100.0	559	4	AAK94018	Aak94018
G	24	100.0	559		ADI.30445	Ad13044

Description	Aac64409 Human Nod	Aac07129 Human sec	Aak92844 Human cDN	Ad129271 3' end of	Aak94018 Human cDN	Adl30445 3' end of	Adg63407 Partial h	Aax04379 Human sec	Aaz36230 cDNA enco	Aad08386 Human sec	Aak94408 Human ful	Adl31137 Full leng	Aaf32725 Human sec	Adk14166 Human aut	Abv94681 Human pan	Aac64406 Human Nog	Aav30920 Human sec	Aaf98399 Human cDN	Adol5813 4 synthes	Adp45550 Human Nog	
ΩI	AAC64409	AAC07129	AAK92844	ADL29271	AAK94018	ADL30445	ADG63407	AAX04379	AAZ36230	AAD08386	AAK94408	ADL31137	AAF32725	ADK14166	ABV94681	AAC64406	AAV30920	AAF98399	AD015813	ADP45550	
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Query Match Length DB	24	496	536	536	559	559	972	1213	1610	1683	1694	1694	1758	1785	2235	2240	2386	2386	2512	3919	
Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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AAC81048 Human CDN AAC811048 Human Nog AAD13574 Renal cel AAA23454 CDNA enco AAA94680 Human pan AAA34563 Human mad AA104697 Human rep AA104697 Human rep AA107604 Human rep AA107604 Human rep AA107604 Human neu AA870499 Human neu AA870499 Human neu AA829079 CDNA enco AA872191 CDNA enco AA82213 Human CDN AA829151 CDNA enco AA625213 Human CDN AA829151 CDNA enco AA625213 Human CDN AA829151 CDNA enco AA625285 Human CDN AA872193 Human CDN AA872193 Human CDN AAN72193 Human CDN AAN732193 Human CDN	Human Human Human
AAS09453 ACC81048 ADP13574 AAA23454 ABV94680 ADG32772 ABC32772 ABC32772 ABC32772 ABC32772 ABC327449 ABC70449 ABC70449 ABC73499 ABC25013	ABV49730 ABV19969 AAH71132
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4053 4063 4063 4632 4710 4710 4822 25 21 21 21 360 360 360 360 360 377 377 377	602 633 702
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4 4 4 4 4 4 4 4 4 4 4 4 4 0 0 0 0 0 0 0	555
12000000000000000000000000000000000000	4 4 4 5 4 5
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ALIGNMENTS

RESULT 1 AAC64409

AAC64409 standard; RNA; 24 BP.

AAC64409;

08-FEB-2001

(first entry)

Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:5.

Human, Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth, cellular stress response; neuron growth, regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; antisense;

Homo sapiens.

phosphorothioate; ss.

 .24
 /*tag= a
 /note= "phosphorothioate linkages" Location/Qualifiers Key modified_base

WO200060083-A1

12-OCT-2000.

07-APR-2000; 2000WO-US009383

99US-0128372P. 08-APR-1999; 21-JUN-1999;

(CHIR) CHIRON CORP.

Williams LT; Halenbeck R, Wei D,

WPI; 2000-665007/64.

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

procedures.

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Matches
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                       The present invention describes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polymucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, 5' EST; expressed sequence tag; secreted protein, cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                     identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligonucleotide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                       100.0%; Score 24; DB 3; Length 24; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                              Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 11204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                      AUCCACCAGUGCCUCAGAUAGGA 24
                                                                                                                                                                                                                                                                                                                   1 AUUCCACCAGUGCCUCAGAUAGGA 24
 Claim 25; Page 32; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      AAC07129/c
ID AAC07129 standard; cDNA; 496 BP
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45.
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Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                                                                                                                                      Gaps
diagnostic, forensic, gene therapy and chromosome mapping procedures
They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K, Ishii S, Kawai Y;
K, Kojima S, Otsuki T, Koga H;
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                                                                                                                                                           ; Score,24; DB 3; Length 496;
Pred. No. 0.19;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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                                                                                                                Sequence 496 BP; 156 A; 77 C; 104 G; 158 T; 0 U; 1 Other;
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Wakamatsu A, Sugiyama T, Nagai
                                                           expression and secretion vectors
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                                                                                                                                                                      100.0%;
79.2%; E
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK92844 standard; cDNA; 536
                                                                                                                                                                   Query Match
Best Local Similarity 79.29
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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hes 19; Conservative
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ADL2927

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The invention relates to primers for synthesising full length cDNA and cules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                  Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; SEQ ID NO 2478; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 4; Length 559; 79.2%; Pred. No. 0.2;
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    end of a representative human cDNA cluster SegID 2478.

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                                                                                                                                    07-JUL-2000; 2000EP-00114089.
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
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02-MAY-2000; 2000JP-00183765
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Best Local Similarity 79.2%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      in genetic manipulation.
                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-524255/58
  Homo sapiens.
                                          EP1130094-A2
                                                                                                                                                                                 08-JUL-1999;
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                                                                                       05-SEP-2001
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ADL30445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polymuclectide sequence is the 3' end of a full length human cDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                     signal transduction; glycoprotein; transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA clone representative sequence, SEQ ID NO: 2478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 536 BP; 169 A; 120 C; 92 G; 148 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1304; 1340pp; English
                                                                                                                                                                                                                      3' end of a human cDNA molecule SegID 1304.
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                                                                                    ADL29271 standard; cDNA; 536 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAX-2000; 2000JP-001183865.
07-JUL-2000; 2000EP-00114089.
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                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                           oligo-capping method; ss.
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                                                                                                                                                                                                                                                                     human; medicine;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                               ADL29271;
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12-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                         New oligonuclectide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
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/note= "Deletion associated with CAA polymorphism"
replace (725. .729,cc)
/*tag= "Polymorphism"
                                                                               Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; human; neuropsychiatric disorder; Nogo polymorphism; Nogo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 12; Length 559; 79.2%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 559 BP; 178 A; 129 C; 94 G; 152 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                        Example 18; SEQ ID NO 2478; 1340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG63407 standard; cDNA; 972 BP
                                          RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2002; 2002GB-00011212
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    07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism; schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial human Nogo cDNA.
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(TALL/) TALLERICO T.
                                                                                                                                          WPI; 2004-204755/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003215868-A1
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                                            (REAS-)
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                                                                                                                                                                         patient to a neuropsychiatric disorder, comprising obtaining a sample from a patient, and testing the sample for the presence of a polymorphism in the Nogo gene, where the presence of a polymorphism indicates that the patient is susceptible to a neuropsychiatric disorder. The method is useful for determining the susceptibility of a patient to a neuropsychiatric disorder e.g. schizophrenia. The present sequence represents human Nogo partial cDNA.
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                                                                                                                                                  The invention relates to a method of determining the susceptibility of
Determining susceptibility of patient to neuropsychiatric disorder, by obtaining sample from patient, and testing the sample for presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.22;
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                                                                                                        Claim 2; SEQ ID NO 1; 12pp; English
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970S-0049550P-
970S-0049566P-
970S-0049606P-
970S-0049608P-
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97US-0058665P.
97US-0058668P.
97US-0058669P.
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97US-0050901P.
97US-0052989P.
97US-0051919P.
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79.2%; F
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                                    obtaining sample from pati
polymorphism in Nogo gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 19; Conserv
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin for portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novell genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Dased on which tissues are described for each of the
                                                                                                                                                                                                                              Ni J;
                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                              Olsen HS;
                                                                                                                                                                                                                                 Yu G,
                                                                                                                                                                                                                          Sbner R, Brewer LA, Young P, Greene JM, Ferrie AM,
                                                                                                                                                                                                            Lafleur DW,
                                                                                                                                                                                                            Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 235-236; 380pp; English.
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                                                                97US-0060841P.
97US-0060844P.
97US-0060865P.
97US-0061059P.
97US-0058971P.
97US-0058972P.
97US-0058975P.
97US-0060834P.
                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                            WPI; 1999-080881/07.
P-PSDB; AAW78194.
                                                                                                                                                                                                        Shi Y,
              12-SEP-1997;
12-SEP-1997;
02-OCT-1997;
                                                                                  02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
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                     Score 24; DB 2; Length 1213;
Pred. No. 0.22;
Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 0 U; 4 Other;
                                               0; Indels
                                               5; Mismatches
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                       100.0%;
79.2%; P
                                               Conservative
        Query Match
Best Local Similarity
19; Conserve
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1079 ATTCCACCAGTGCCTCAGATAGGA 1056
        RESULT 9
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Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; lymphoid cell deficiency; lymphoid cell deficiency; granulocyte; morophage; myelo: colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint; ss. cDNA encoding a bone marrow secreted protein designated BMS112.

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Excessory sector bound marrow sectored processing of the proteins can exhibit cytokine, cell proliferation, or strongl cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell lines, to proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prowntion or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bour cartilage. Compute the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bour cannot healing and tissue repair and replacement, and in the treatment of burns, incisions can ulcers, to induce cartilage and/or bone growth in circumstances where be not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture caucition and also in the improved fixation of artificial joints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ36228-49 encode bone marrow secreted proteins of human bone marrow
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                                                   /*tag= a
/product= "bone marrow secreted protein"
1516. .1521
/*tag= b
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               Location/Qualifiers
132. .1253
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98US-0101603P.
98US-0102540P.
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                                                                                                                                                                                                                                                                                                                                                                                   Cao L;
                                                                                                                                                   WO9933979-A2
                                                                                                                                                                                                                            18-DEC-1998;
                                                                                           polyA_signal
                                                                                                                                                                                                                                                                30-DEC-1997;
24-SEP-1998;
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ID AAD083
XX
AC AAD083
XX
DT 09-AUG
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XXX
XWW Huma
XXX Huma
XXX KWW infil
XWW infil
XWW infil
XWW gast KWW gast K

Human secreted protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52.

Human; secreted protein; proliferative disorder; cancer; tumour; fucetal abnormality; hammatopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson; disease; capmitive disorder; schizophrenia; sthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;

Homo sapiens.

WO200077022-A1.

21-DEC-2000.

01-JUN-2000; 2000WO-US015136.

11-JUN-1999; 99US-0138629P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM, Komatsoulis GA;

WPI; 2001-367020/38. P-PSDB; AAE03939. Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.

Claim 1; Page 520; 614pp; English.

AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03998-AAE03947 represent the protein steps encode. AAE03996 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the conversion of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, connected disorders, schizophrenia, asthma, skin disorders (e.g., rheumatoid arthritis), inflammation, allergies, connitive disorders, schizophrenia, asthma, skin disorders (e.g., angiogenic disorders, altered schizophrenia, anthritian disorders, angiogenic disorders, indoction asthma, skin disorders, angiogenic disorders, indoction asthma, skin disorders, angiogenic disorders, and sorders, and sorders, angiogenic disorders, and sorders, and sorders, proteins can also be used to aid wound healing and epithelial call proliferation, to prevent skin aging due to surburn, to maintain organs to regenerate tissues, to identify their cognate ligands or binding to regenerate tissues, and can be used as a food additive or

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Gaps

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; Score 24; DB 4; Length 1694; Pred. No. 0.23; 5; Mismatches 0; Indels (

100.0%; 79.2%; F

Local Similarity 79.2

Matches

Query Match

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preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                     Gaps
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T, Koga H;
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                                                                                                                                                   Score 24; DB 4; Length 1683; Pred. No. 0.23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
                                                                                                                 Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                     Indels
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K, Kojima S, Otsuki
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                                                                                                                                                                                     5; Mismatches
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IA T, NAGAİ
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                                                                                                                                                                                                                                                                                                                                    AAK94408 standard; cDNA; 1694
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                    100.08;
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                                                                                                                                                                    ilarity 79.2%;
Conservative
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                                                                                                                                                                     Local Similarity
Les 19; Conserv
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                                                                                       invention
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                                                                                                                                                        Query Match
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Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;

Human secreted protein gene 27 SEQ ID NO:37.

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This invention relates to a novel primers useful for synthesising full length CDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, encoding proteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                           human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ai T, Hayashi K, Ishii S, Kawai Y;
Nagai K, Kojima S, Otsuki T, Koga H;
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Pred. No. 0.23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 3170; 1340pp; English.
                                                                                                                                                                                                 Full length human cDNA clone SeqID 3170.
            1 AUUCCACCAGUGCCUCAGAUAGGA 24
                                                                                                       ADL31137 standard; cDNA; 1694 BP
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79.2%; F
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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                                                                                                                                                                    (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length human cDNAs
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                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                    20-MAY-2004
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                                                                                                                                     ADL31137;
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The polymucleotide sequences given in AAP32699 to AAF32747 encode the human secreted proteins given in AAB64422 to AAB64470. AAB64471 to AAB64471 to AAB64458 represent human secreted polypeptide sequences and proteins howologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues cand cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; creebroprotective; nootropic; cardiant; vasotropic; creebroprotective; nootropic; creebroprotective; notroprotective; antibacterial; virucide; fungicide; and optimal polymucleotides and polymptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to pathological condition. Disorders or susceptibility to a also used autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative catiac arrest, creebrovascular disorders e.g. cardiac arrest, creebrovascular disorders e.g. cardiac arrest, creebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound chaing and epithalial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting colluture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAF32690 to AAF32690 and AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF32690 to AAF3
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                                                                                            antitheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fugicide; ophthalmological; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebrovascular disorder; erebrai system disorder; Alzheimer's disease; skin aging; ocular disorder; corneal infection; wound healing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000; 2000WO-US014926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0138628P.
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                                                                                                                                                                                                                                                                                 preservative; ss
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                                                                                                                                                                                                                                                                                                                                                                                WO200077255-A1.
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Gaps

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Indels

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5; Mismatches

19; Conservative

Matches

24

1619 ATTCCACCAGTGCCTCAGATAGGA 1596

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AAF32725 standard; cDNA; 1758 BP

RESULT 13

23-MAR-2001 (first entry)

AAF32725;

1 AUUCCACCAGUGCCUCAGAUAGGA

Pred. No.

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New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                            30-JAN-2001; 2001US-0265305P.
31-JAN-2001; 2001US-0265682P.
00-FEB-2001; 2001US-0267568P.
21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-033184P.
20-AUG-2001; 2001US-03139999P.
                                                                                                            30-JAN-2002; 2002WO-US002781
                                     WO200260317-A2
Homo sapiens.
                                                                          08-AUG-2002
The invention relates to a method of detecting an autoimmune disorder in a subject comprising obtaining a biological sample, preferably a peripheral blood mononuclear cell, from a subject, determining expression levels of at least two genes in the biological sample, and comparing the expression level of each gene ermined with a standard, where the comparison detects the presence of an autoimmune disorder in the subject. The method is useful for detecting or diagnosing an autoimmune disorder, e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple solerosis, or type 1 (insulin-dependent) diabetes. The present sequence represents one of seventy genes used to detect autoimmune disorders with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting an autoimmune disorder in a subject comprising comparing the expression level of each gene determined with a standard, where the comparing detects the presence of an autoimmune disorder in the subject.
                                                                                                                                                                                                       gene; ss; autoimmune disorder; peripheral blood mononuclear cell; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; type 1 (insulin-dependent) diabetes; human.
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5; Mismatches
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                                                                                                                                                                         Human autoimmune disorder gene #62
                                                             ADK14166 standard; cDNA; 1785 BP.
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Best Local Similarity 79.2%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2002; 2002US-0381055P
                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the described method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen NJ;
                                                                                                                                                                                                                                                                                                                             JS2003228617-A1
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                      06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                    11-DEC-2003
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                                                                                                    ADK14166;
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for

Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.

Persing DH, Hepler WT, Jiang Y;

Lodes MJ,

Kalos MD,

Benson DR,

(CORI-) CORIXA CORP.

WPI; 2002-627435/67.

P-PSDB; ABP68601

cancer.

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The invention relates to an isolated polymucleotide (I) comprising: (a)

any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

camplements of (a); (c) sequences consisting of at least 20 contiguous

complements of (a); (d) sequences that hybridize to (a), under moderately

cresidues of (a); (d) sequences having at least 75 or 90% identity

cresidues of (a); (d) sequences having at least 75 or 90% identity

cresidues of (a); (l) and oligonucleotides (ABP66596-

couls expressing the oligonucleotides, polymucleotides,

antibodies, fusion proteins, T cell populations and antigen presenting

calls expressing the polypeptide are useful in treating pancreatic cancer

and stimulating an immune response. The polymucleotides can be used as

probes or primers for nucleic acid hybridisation, in the design and

probes or primers for nuclein and thybridisation, in the design and

probes or primers for nuclein and the tumour cells, in vaccines and for gene

conference of therapy. Note: The sequence data for this patent did not form part of the

conference of the capanish of the tumour cells, man and the conference of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;
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Gaps

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1078 ATTCCACCAGTGCCTCAGATAGGA 1055

ABV94681 standard; cDNA; 2235

RESULT 15

1 AUUCCACCAGUGCCUCAGAUAGGA 24

ઠે 셤 Human; pancreas; cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss.

Human pancreatic cancer expressed cDNA SEQ ID NO 54.

(first entry)

14-JAN-2003

ABV94681/ 1D ABV9 XX ABV9 XX ABV9 XX 14-J DT 14-J XX Huma XX Huma XW Cyto

ABV94681;

AA236753 zr99g11.r AW46808 health05.x AA236111 ze05e02.x AA236111 ze05e12.r T34669 EST73062 Hu AV708414 AV708414 AV708414 BW42235 AGENCOURT BE172028 MRO-HT055 AA044644 Zn2206.8 AA159037 ze57406.8 AA159037 ze57406.8 AA41293 AV648293 AV648293 AV648293 AN648219 AV648293 AN648219 AV648293 AN648219 AV648293 AN648219 AV648293 AN648293 ZC19e11.r1 AA235659 ZC1311.r1

36753 58088 74377 74377 79315 79315 79315 79316

C 25 24 100.0 312 1 AA236 26 24 100.0 321 2 AW466 27 24 100.0 322 1 A1874 C 28 24 100.0 341 1 AA236 29 24 100.0 341 1 AA236 31 24 100.0 350 1 A1246 31 24 100.0 351 5 BU6875	24 100.0 352 7 24 100.0 353 1 24 100.0 354 4	36 24 100.0 365 1 37 24 100.0 379 1 38 24 100.0 379 1 38 24 100.0 382 1 38 24 100.0 386 4	40 24 100.0 386 7 41 24 100.0 390 1	24 100.0 396 1 24 100.0 396 1 24 100 0 397 7	45 24 100.0 400 1	AI	RESULT 1 A1216602	ITION	z	KEYWORDS EST. SOURCE Homo sapiens (human)	~	RS AL	COMMENT Contact: Robert Strausberg Email: cgapbs-r@mail.nih.g	Tissue Procurement: Christ Emmert-Buck, M.D., Ph.D. CONA Library Preparation:	DNA Sequencing by: Washin Clone distribution: NCI-C	<pre>tound through the I.M.A.G. www-bio.llnl.gov/bbrp/imag</pre>	Insert Length: 965 Std E Seg primer: -40UP from Gib	FEATURES Location/Qualifie	,	/db_xref="taxon:9 /clone="IMAGE:188	/tissue_type="car /lab host="DH108"	/clone_lib="NCI_C /note="Organ: lun	modified polylink neuroendocrine lu	Not I - oligo(dT) to Eco RI adaptor	pT7T3 vector. Lip	ORIGIN
GenCore versio pyright (c) 1993 - 2005 search, using sw model	Run on: July 30, 2005, 11:50:11; Search time 2458.7 Seconds (without alignments) 371.555 Million cell updates/sec	Title: US-09-544-776-5 Perfect score: 24 Sequence: 1 auuccaccagugccucagauagga 24	Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0	Searched: 34239544 segs, 19032134700 residues	Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	BS :			95_est6:* 95_gss1:* gb_gss2:*	s the number of results predicted by chance to have a er than or equal to the score of the result being printed, ved by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	24 100.0 125 24 100.0 127	24 100.0 174 2 BE620536 24 100.0 176 7 T30356	5 24 100.0 179 5 BU963350 6 24 100.0 195 4 BG271724	24 100.0 196 7 F00105 24 100.0 207 7 238593	9 24 100.0 209 1 AA252742 0 24 100.0 237 1 AA989076	11 24 100.0 245 2 AW148462 12 24 100.0 247 1 AT796628	3 24 100.0 258 7 TB2303 4 24 100.0 262 6 CD368992	5 24 100.0 267 2 BF734642 6 24 100.0 281 4 BG170953	7 24 100.0 287 7 F10097 8 24 100.0 287 7 F10120	287 7 T54784 T54784 289 7 T35248 T33248 200 1 N176610 NN17661	2 24 100.0 295 4 BG121948 3 24 100.0 301 1 AA906723	4 24 100.0 305 7 W46607 W46607

LIGNMENTS

35659

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/tissue type="carcinoid"
/lab_host="blub"
/clone lib="NCI CGAP Lus"
/clone lib="NCI Lib strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. " ion: M. Bento Soares, Ph.D.
by: Greg Lennon, Ph.D.
sahington University Genome Sequencing Center
(IncGAP Clone distribution information can be
'image/image.html
'image/image.html
'ighthere'
'ighthere'
'ighthere'
'ighthere'
'ighthere' 125 bp mRNA linear EST 02-DEC-1998 domo gapiens cDNA clone IMAGE:1883600 3', lata; Craniata; Vertebrata; Buteleostomi; .gov stopher Moskaluk, M.D., Ph.D., Michael R. .nlm.nih.gov/ncicgap. e, Cancer Genome Anatomy Project (CGAP), tes; Catarrhini; Hominidae; Homo. Ph.D. sapiens" .9096 ORIGIN ö

Gaps

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Indels

Query Match

Matches

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

MEDLINE PUBMED COMMENT

JOURNAL

DEFINITION

RESULT 2 BM725018

ACCESSION

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5; Mismatches
                                                                 1 AUUCCACCAGUGCCUCAGAUAGGA 24
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                                           1 AUUCCACCAGUGCCUCAGAUAGGA
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/ organism="Homo sapiens"
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/ db xref="taxon:9606"
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U1-E-E01 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1966. First strand cDNA synthesis was primed with an oilgo-dr prime containing a synthesis was primed with an oilgo-dr prime containing a hot I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector: The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGTATACC: This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                                                                                   EST 01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa 157 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 8250
Fax: 319 319 355 9565
Email: bento-soares@uiowa.edu
Tisue Procurement: Dr. Gregg Hageman
Tisue Procurement: Dr. Gregg Hageman
TONA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa CLONE Distribution: Researchers may obtain clones from Research Genetics (www.reseen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                      Gaps
                                                                                                                                                                                                                                                                              UI-E-EO1-aja-i-18-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone UI-E-EO1-aja-i-18-0-UI 5', mRNA sequence.
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                        DB 1; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB Coordinated Laboratory for Computational Genomics
                                                                      0; Indels
                        100.0%; Score 24; DB 79.2%; Pred. No. 2; ive 5; Mismatches
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source

FEATURES

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T30356 176 bp mRNA linear EST 06-SEP-1995 EST15349 Human Endothelial cells Homo sapiens cDNA 5' end similar to None, mRNA sequence.
BE620536 174 bp mRNA linear EST 20-OCT-2000
601483007T1 NIH_MGC_69 Homo sapiens CDNA clone IMAGE:3885864 3',
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
site_2: SalI; Cloned unidirectionally. Drimer: Oligo dT.
mobbodicae insert size 1.1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9661 row: m column: 01
High quality sequence start: 27
High quality sequence start: 27
High quality sequence stop: 158.
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                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 174)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG271724.1 GI:12980154
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AUTHORS
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BG271724
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Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earlé-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Pritchman, J.L., Geoghagen, N.S.M., Kelley, J.W., Kilmek, K.M., Kelley, J.L., Liut, L.T., Marmaros, S.M., Merzick, J.W., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Warmaros, S.M., Weidman, J.F., Li, Y., Badnarik, D.P., Cooleman, T.A., Collins, E.-J., Dimke, D., Ferigy, P., Ferrie, A., Gruber, J., Hudson, P., Kim, A., Mosson, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Kunsch, C., Ji, H., Li, H., Haseltine, W.A., Fleids, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          את 179 bp mRNA linear EST 21-OCT-2002 AGENCOURT 10616090 NIH MGC 141 Homo sapiens cDNA clone IMAGE:6744396 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 179)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 24; DB 7; Length 176; Best Local Similarity 79.2%; Pred. No. 2.2; Matches 19; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="endothelial"
/clone_lib="Human Endothelial cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="ATCC (inhost):100067"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other ESTs: THC11414
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 176
/organism="Homo sapiens"
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Tissue Procurement: NCI
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/ucydallaries mount Beatherns.
/wol types | mRNA |
/db_xref="taxon:9606"
/dlone="THAGE:6744396"
/foloe="THAGE:6744396"
/foloe="THAGE:6744396"
/foloe="THAGE:6744396"
/foloe="THAGE:6744396"
/foloe="DH10B (T1-phage-resistant)"
/foloe="DH10B (T1-phage-resistant)"
/foloe="Upercor: pDNR-CL1B; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder-2%, blood -33.4%, brain -5.6%, breast -12.5%, colon-4%, connective tissue -1.4%, eye -1%, incestine -2.6%, kidney -2.2% liver -5.7%, lung -10.8%, NK-cell -5.2%, connective tissue -1.3%, prostate -4.3%, salivary gland -1.3%, and skin -2.3%). S' and 3' adaptors were used in cloning as follows:
5'-AAGCGGGGACGGCGCGCGACATACGGCGGG-3' and 5'-AAGCGGGGCGCGCGCGCCAATAGGT (30) NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH MGC 142). Library created in the laboratory of M. Brownsteln (NIMH, NIH). Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llhl.gov
Plate: LLCM3085 row. j column: 11
High quality sequence stop: 179.
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                                                                                                                                                                                 /organism="Homo sapiens"
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Query Match

ORIGIN

Matches

ઠ 셤 LOCUS

RESULT 7 F00105/c

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

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/tissue type="total brain"
/tissue type="total brain"
/dev stage="3 months old"
/clone lib="normalized infant brain cDNA"
/clone lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev stage=3 months old;
Site_2: NotI; sex=Female; dev stage=3 months old;
Site_2: NotI; sex=Female; dev stage=3 months old;
brain; ctotal mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector: Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
                                                                                                                               207 bp mRNA linear EST 31-OCT-1994 HSCOHBO82 normalized infant brain cDNA Homo sapiens cDNA clone c-Obbo8 3', mRNA sequence.
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2826a12.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686302 5',
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Single read. 18 T removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-0hb08
Seq primer: (-21)M13 universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 BVRY Cedex, FRANCE
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                         Z38593.1 GI:560985
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Best Local Similarity 79.24
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence. —
AA252742
AA252742.1 GI:
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AA252742/c
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   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                             /clone_lib="NCI_CGAP_HN20"
/clone_lib="NCI_CGAP_HN20"
/clone="Organ: normal head/neck tissue; Vector: pAMP1; mRNA
made from head/neck tissue, cDNA made by oligo-dr
priming. Directionally cloned into UDG sites.
Size-selected on agarose gel, average insert size 300 bp.
Primary library. cDNA Library Preparation: David B.
Krizman, Ph.D.
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/dev_stage="19 years"
/clone_lib="GTRATAGENE Human skeletal muscle cDNA library,
cat. #916215."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotacia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea I to 196)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Sebastiani-Kabaktchis, C. and Tessier, A.

Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
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HSB21G041 STRATAGENE Human skeletal muscle cDNA library, cat.
#396215. Homo sapiens cDNA clone 21G04, mRNA sequence.
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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95277534
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Single read.
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Location/Qualifiers
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F00105.1 GI:707366
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AW148462.1 GI:6196358
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0208602.sl NCI_CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1602938 3',
              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
I (bases 1 to 209)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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NCI-Case http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thunor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tanmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 210
Insert Length: 718 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp//amage/image.html
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High quality sequence stop: 208.
Location/Qualifiers
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DRIGIN

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Tumor Gene Index
To Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
BollyA=Yes.
                                                            T82303 258 bp mRNA linear EST 30-JAN-2001 AS267 Subtracted human retina Homo sapiens CDNA clone AS267 3',
                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 258) 1 (bases I to 258) 2 (bases I to 258) 2 (bases I to 258) 2 (bases I to 258) 2 (bases) 1 (bases) 1 (bases) 1 (bases) 1 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bases) 2 (bas
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Department of Ophthalmology and Visual Sciences
Kellogg Eye Center, University of Michigan
540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
Tel: 734 647 0228
Email: swaroop@umich.edu
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                                                                                                                                                                                                    T82303.1 GI:705310
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I Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 330 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Ind_note="Univo"
/clone_lib="NUIC CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site=1: Not 1; Site=2: ECo R1;
Plasmid DNA from the normalized library NCT CGAP Kid3 was
prepared, and so circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 13223/6-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
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/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 247)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                        2; Length 245;
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                                                                                                                                                                                                           Score 24; DB
Pred. No. 2.3;
                                                                                                                                                                                                    ch 100.0%; Score 24; DB Similarity 79.2%; Pred. No. 2.3; 19; Conservative 5; Mismatches
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5; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2384976"
/lab_host="DH10B"
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                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
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Matches

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DRIGIN

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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COMMENT

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ACCESSION

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RESULT 12 AI796628

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//note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: ECR I; Site_2: Not I;

NCI_CGAP_FTI is a normalized CDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages explailenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)
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1 (bases 1 to 267)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harce, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                           /clone="UI-H-FTI-bjx-f-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                organism="Homo sapiens
                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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TAG_SEQ=GGCCATGCCG"
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AUTHORS
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/dev_stage="Adult"
/clone llb="AN0068"
/clone llb="AN0068"
/note="Organ: amnion normal, Vector: puc18; Site_l: Smal;
Site_l: Smal; A mini-library was made by cloning products
Site_l: Smal; A mini-library was made by cloning products
Geriyed from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                               Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-AN0068-
301100-012-Bli&ts3=2000-11-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 244.
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                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                      Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Search completed: July 30, 2005, 15:01:03 Job time : 2461.7 secs

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TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. 0.033;
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; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL PROGram
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1 LOCATION: 486

7 CTHER INFORMATION: n=a, g, c or t

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Best Local Similarity 79.2
Matches 19; Conservative
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US-09-023-655-382/c
US-09-023-655-382/c

| Sequence 382, Application US/09023655
| Patent No. 6607879
| GENERAL INFORMATION:
| APPLICANT: Cocks, Benjamin G. Stuart
| APPLICANT: Susan G. Stuart
| TITLE OF INVENTION: EXPRESSION |
| TITLE OF INVENTION: EXPRESSION |
| TITLE OF INVENTION: EXPRESSION |
| TORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: INCTE PHARMACEUTICALS, INC. |
| STREET: 3174 PORTER DRIVE |
| CITY: PALO ALTO |
| STATE: CALIFORNIA
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Pred. No. 0.4;
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.7%; Score 22; DB 4; Best Local Similarity 77.3%; Pred. No. 0.43; Matches 17; Conservative 5; Mismatches
                                                                                                                                                                                                                                                              5; Mismatches
            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3253
LENGTH: 1669
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNDRER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           Query Match
Best Local Similarity 77.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2610 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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; CLONE: 1508778
US-09-023-655-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line
                                                                                                                                    , ORGANISM: Human
US-09-949-016-3253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                               TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 2000-04-14, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
                                                                                                                                                        ; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106
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APPLICANT: Prashar, Yatindra
APPLICANT: Prashar, Yatindra
APPLICANT: Newberger, Peter
APPLICANT: Newberger, Peter
APPLICANT: Weiseman, Sherman M.
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
FILE REFERENCE: 44921-5016-US
CURRENT APPLICATION NUMBER: US/09/506,729
CURRENT FILING DATE: 1998-08-21
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 211
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100.0%; Score 24; DB 3; Length 4822;
Best Local Similarity 79.2%; Pred. No. 0.05;
Matches 19; Conservative 5; Mismatches 0; Indels C
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                                                                                        FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
                                                                                                                                                                                                                                                                                                                                                                                                                      4099 ATTCCACCAGTGCCTCAGATAGGA 4076
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; Sequence 3253, Application US/09949016
; Patent No. 6812339
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; Sequence 51, Application US/09506729
; Patent No. 6365352
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Best Local Similarity 77.3'
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                    LENGTH: 4822
TYPE: DNA
ORGANISM: Homo sapiens
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SEQ ID NO 106
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2148 ATTCCACCAGTGCCTCAGATAG 2127

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Sequence 17019, Application US/09949016

Sequence 17019, Application US/09949016

Ratent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPREMENCE: CLOORD.307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREEKER ERSESED for Windows Version 4.0

SEQ ID NO 17019
                                                                PAPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERBNCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PEALSEQ for Windows Version 4.0

LENGTH: 601
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66.7%; Pred. No. 13;
tive 5; Mismatches
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78.3%; Score 18.8;
Best Local Similarity 72.7%; Pred. No. 3:
Matches 16; Conservative 4; Mismatch
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Sequence 7041, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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US-09-949-016-17020/c
; Sequence 17020, Application US/09949016
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.73
Best Local 16, Conservative
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ORGANISM: Human
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ORGANISM: Human
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US-09-949-016-31983/C

Sequence 31383, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-00-41,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-09

PRIOR FILING DATE: 2000-00-09

NUMBER OF SEQ ID NOS: 207012

SEQTYMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 31983
                                                                                                   Geguence 14995, Application US/09949016

gequence 14995, Application US/09949016

general No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWAR: FRASESQ IO Windows Version 4.0

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LEACTH: 4.2075
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Pred. No. 0.72;
5; Mismatches
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Best Local Similarity
Matches 17; Conserv
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US-09-949-016-70441/c
                                                                                              US-09-949-016-14995/c
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US-09-949-016-14995
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ORGANISM: Human
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NAME/KEY: misc_feature
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US-09-949-016-11852/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION:
GURRENT ELING DATE: 2000-04-14
CURRENT PELICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17021
LENGTH: 246230
GENERAL INFORMATION:
GENERAL INFORMATION:
JENERAL APPLICATION NUMBER:
JENERAL A
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Pred. No. 38;
4; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134516 TTCCACCAGTGCCTCAAACAGG 134495
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US-09-949-016-17021/c
; Sequence 17021, Application US/09949016
; Patent No. 6812339
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    OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17020
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) LOCATION: (1)...(246230)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17021
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Best Local Similarity 72.7%;
Matches 16; Conservative
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ORGANISM: Human
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134516 TTCCACCAGTGCCTCAAACAGG 134495

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Sequence 11852, Application US/09949016
; Sequence 11852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VBYTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TURENT APPLICATION NUMBER: US/09/949,016
; CURRENT PLING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-010-03
sequence 17022, Application US/09949016

j Batent No. 6812339

j GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION UNMBER: US/09/949,016
   CURRENT APPLICATION NUMBER: 00/241,755
   PRIOR PELING DATE: 2000-10-20
   PRIOR PELING DATE: 2000-10-30
   PRIOR PILING DATE: 2000-10-03
   PRIOR PILING DATE: 2000-10-03
   PRIOR PILING DATE: 2000-10-03
   NUMBER OF SEQ ID NOS: 207012
   SOUTHARE: PRESE EASTESQ for Windows Version 4.0
   SEQ ID NO 17022
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Best Local Similarity 80.0%; Pred. No. 63;
Matches 16; Conservative 3; Mismatches
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72.7%; Pred. No. 38;
tive 4; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11852
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| LOCATION: (1)...(246230)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17022
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Best Local Similarity 72.7*
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287950 TCCACCAGTGCCTCAGAGAG 287931

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Sequence 16654, Application US/09949016

Sequence 16654, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
PILE REPERENCE: CLOOD 307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PLLING DATE: 2000-010-03

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOOTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16654

LENGTH: 64593
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65.2%; Pred. No. 59;
:ive 5; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14166
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| LOCATION: (1)...(64593)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16654
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Best Local Similarity 80.0%;
Matches 16; Conservative
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Best Local Similarity 65.2
Matches 15; Conservative
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US-09-949-016-16654/c
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ORGANISM: Human
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ORGANISM: Human
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LENGTH: 321022
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                           CQ76366 Sequence
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 561 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers

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/organism="synthetic construct"
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other sequences; artificial sequences.
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Sequence 1429 from Patent W00159103.,
AX215987
AX215987.1 GI:15526030
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Sequence 561 from Patent W00159103.
AX215119
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CQ762483
CQ763482
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AX650316
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AX216585
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A92752
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AX215119/C
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CQ815775
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AX401760
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                     - nucleic search, using sw model
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AX216842
AX481558
AX216586
CQ535926
AX225975
AX160170
AX215989
CQ537946
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CQ816744
AR401760
AX722986
BD067260
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Listing first 45
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 2284 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
MCSwiggen, James (US) ; Chowrira, Bharat M. (US)
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nogo gene expression
Patent: WO 0159103-A 1737 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 2029 from Patent WO0159103.
AX216587
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Matches 12; Conservative
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AX216842/c
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                                                  Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1429 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1430 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 1.6e+03;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db xref="taxon:32630"
/noTe="Nucleic Acid"
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Sequence 1430 from Patent WO0159103.
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Sequence 1737 from Patent WO0159103.
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Best Local Similarity 76.5%;
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AX215988/c
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TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
Patent: WO 0210449-A 5561 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                 Blatt, L., Mcswiggen, J. and Chowrira, B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression Patent: WO 0159103-A 2028 16-AUG-2001; RIBOZYMS PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
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 Length
 Score 16.4; DB 6;
Pred. No. 3.3e+03;
3; Mismatches 1;
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68.8%; Pred. No. 5.3e+03;
iive 5; Mismatches 0;
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Sequence 5561 from Patent W00210449.
CQ535926.
CQ535926.1 GI:41502190
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Sequence 2028 from Patent WO0159103.
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/organism="Homo sapiens"
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Location/Qualifiers
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 ch 65.6%;
1 Similarity 77.8%;
14; Conservative
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Best Local Similarity 68.4
Matches 13; Conservative
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   Query Match
Best Local Similarity
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AX216586/c
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humanen EGFR-Sequenz ist"
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komplementar zur humanen EGFR-Sequenz ist"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P. Method for inhibiting the expression of a target gene Patent: WO 02055693-A 173 18-JUL-2002; Ribopharma AG (DE)
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                                                                                                                        Length 17;
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                                                                                                                       68.0%; Score 17; DB 6; I
ilarity 76.5%; Pred. No. 1.6e+03;
Conservative 4; Mismatches 0;
1. .17
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    .24
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    .22
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other sequences; artificial sequences.
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PAT 30-JAN-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                     Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1431 16-AUG-2001;
RIBOZYMS PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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/note="Nucleic Acid"
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Sequence 20410 from Patent W00210449.
CQ550775 GI:41517202
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                                                                     other sequences; artificial sequences.
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Sequence 7581 from Patent WO0210449.

    .60
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    /db_xref="taxon:9606"

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CQ537946.1 GI:41504210
AX215989.1 GI:15526032
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Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Accession number cg43284565"
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Nucleic acids containing single nucleotide polymorphisms

methods of use thereof
methods of use thereof
curagen WO 0140521-A 3498 07-JUN-2001;

Curagen Corporation (US)

Location/Qualifiers
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Unclassified.
1 (bases 1 to 20)
Wyatt,J. and Freier,S.M.
Antinsense modularion of Her-1 expression
Patent: US 6444465-A 38 03-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 76.5%; Pred. No. 1.1e+04; 13; Conservative 3; Mismatches 1;
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Sequence 1431 from Patent WO0159103.
AX215989
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Sequence 3498 from Patent WO0140521.
AX160170
                                                                                        AR225975 20 bp I
Sequence 38 from patent US 6444465.
AR225975.1 GI:27264129
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41 ATCTTGGATCACACCCATG 23
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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DEFINITION ACCESSION

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Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 20410 07-FEB-2002;
Compugen Inc. (US)
                                                                                                                                     1. 60
/organism="Homo sapiens"
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REFERENCE
AUTHORS
TITLE
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Query Match 60.0%; Score 15; DB 6; Length 60; Best Local Similarity 56.5%; Pred. No. 1.8e+04; Matches 13; Conservative 5; Mismatches 5; Indels ð

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Search completed: July 30, 2005, 16:20:38 Job time : 719.243 secs

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_	nucleic - nucleic search, using sw model 1 on: July 30, 2005, 12:18:17; Search time 307.77 Seconds (without alignments) 480.857 Million cell updates/sec	Title: US-09-544-776-3 Perfect score: 25 Sequence: 1 cuggauagcuuggaucacacccuug 25	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 4390206 segs, 2959870667 residues	Total number of hits satisfying chosen parameters: 4316768	Minimum DB seg length: 0 Maximum DB seg length: 60	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : N Geneseq_16Dec04:* 1. geneseq_1880s:* 2. geneseq_1890s:* 3. geneseq_1890s:* 4. geneseq_2000s:* 5. geneseq_2001as:* 6. geneseq_201as:* 7. geneseq_2001as:* 8. geneseq_2003as:* 9. geneseq_2003bs:* 10. geneseq_2003bs:* 11. geneseq_20004as:* 13. geneseq_2004as:* 13. geneseq_2004as:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description	25 100.0 25 3 AAC64407	17 68.0 17 4 ABK01737	111	17 68.0 17 4 ABK02284	8 16.6 66.4 58 10 ADF73036 9 16.6 66.4 58 10 ACD28188	16.4 65.6 22 6 ABV78288 16.4 65.6 24 6 ABV78289	16.2 64.8 26 12 ADH72558 Adh72558 Humar 16 64.0 17 4 ABK02028 Abk02028 Human	15.8 63.2 60 6 ABN32813 15.4 61.6 20 6 AABN35524	15.2 60.8 60 12 ADJ/1265 Human	4 ABK01431 ABK01431 6 ABM47662 ADM47662 6 ABM4833 Abm34833

24 10 ADF79148 Adf79148 PSA PCR p 25 10 ACF04642 Auxine tu 17 2 AAV97320 Aav97320 Human EGF 17 8 ACC63426 Aac63426 Muxine ol 20 12 ADJ1754 Adj17724 Adj17750 Adj1750 Auxisense 20 12 ADJ17838 Adj17838 Auxisense 20 12 ADJ16551 Auxisense 20 12 ADJ16551 Auxisense 20 12 ADJ16551 Auxisense 20 12 ADJ16551 Auxisense 20 12 ADJ16551 Auxisense	10 ADC05670 Adc05670 10 ADC0569 Adc05670 6 ADM3338E ADM3338E	ABN42423 6 ABN42423 6 ABL53901 9 ACK21293 4 AAH91639 AAH91639 2 AAH91639 6 AAH91639 6 AAH91639 6 AAH91639 6 AAH91639 7 AAH91639 7 AAH91639	4 AAN91211 4 AAN91211 6 ABN50365 6 ABN37067	A BEKCO27 ABKCO27 Human 12 ADJ16733 Antis ALIGNMENTS	1; RNA; 25 BP.	rst entry)	phosphorothioate antisense oligonucleotide SEQ ID NO:3.	bil stress response; hyperphosphorylated; brain tumour; lated endoplasmic reticulum protein; cytostatic; ll growth; cellular stress response; neuron growth; dative stress; inhibitor of neurite outgrowth; i diagnosis; cancer; identification; antisense;		Location/Qualifiers 125 /*tag= a /note= "phosphorothioate linkages"			000WO-US009383.	3US-0128372P. 3US-0140331P.	ORP.	c R, Williams LT;	164.	sociated with cell stress response useful for modulating all growth, diagnosis and treatment of cancer and and for identifying agonists and antagonists.
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	14.4 57.6 1 14.4 57.6	2 14.1 14.2 14.2 14.2 14.2 14.2 14.2 14.	14.2 56.8 14.2 56.8 1 14.2 56.8 1 14.2 56.8	0.4 4 1 14 4 10 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	RESULT 1 AAC64407 ID AAC64407 standard; RNA; XX AC AAC64407;	08-FEB-2001 (first ent)	Human Nogo B phosphorotl	. 4 4 2 3	Homo sapiens.	Key Location modified base 125 /*tag= /note=	WO200060083-A1.	12-OCT-2000.	07-APR-2000; 2000WO-US0	08-APR-1999; 99US-0128 21-JUN-1999; 99US-014	(CHIR) CHIRON CORP.		WPI; 2000-665007/64.	Novel protein associated w stress levels, cell growth malignant growth and for i
0 0 0 0	υυ	υ	00 (υυ	RES AAC ID XX	X E	X 22 3	* 2 2 2 2 2 3	88	(ELLE)	\$ £ \$	£ ¾	PP X	# # # ¥	88 %	F	₹ 8 \$	ដ្ឋម្

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                                The present invention describes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cycostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neutrite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polymorlocides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ss, antisense therapy, cytostatic, antiinflammatory, haemostatic, cerebroprotective, nootropic, neuroprotective, antiparkinsonian, muscular, CD20, neurite growth inhibitor gene, NOGO, hammerhead ribozyme, DNAzyme; inozyme, G-cleaver; amberzyme; zinzyme; lymphoma, leukaemia; B-cell lymphoma, non-Hodgkin's lymphoma, NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
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                                                                                                                                                                                                                                                      polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligonucleotide from the present invention
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                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;
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Claim 25; Page 32; 68pp; English.
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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(MCSW/)
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The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down corresponded to a cD20 gene and a nucleic acid molecule which down corresponded to a repression of a neurite growth inhibitor gene (NGCO). The nucleic acids and NCH motif), a G-cleaver (cleaving RNA with a NNM motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a NNM motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a NCH with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA correspond to the cell and treat a patient having a condition associated with the level of CD20 in the presence of a divalent cation that is preferably MG^2+. The cast lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-creat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-created lymphoma (NCL), immunocyton argade or follicular NHL, lymphocytic lymphocytic lymphoma, laukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytona (INC), small B-cell lymphocytic lymphoma, contacted with a cell to reduce OCC dargetting nucleic acid may be contacted with a cell to reduce NOCO gene in the presence of a divalent cation that is preferably MG^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOCO gene in the presence of a divalent cation that is preferably MG^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOCO activity of the cell and treat a patient having a condition associated with the level of NOCO. The treatment may further comprise the use of one or more central nervous system (CNS) injury and cerebrowascular accident contacted a disease, dementia, multiple sclerosis (MS), parknow's disease, muscular disease, ataxia, Huntington's disease, created because of the respondent of the nounberties of the respondent of the respondent of the nounberties of the respondent of the 
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constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
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                                                                                                                  Claim 88; Page 74; 200pp; English.
                                                          central nervous system injury.
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Homo sapiens

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The invention relates to a nucleic acid molecule which down regulates expression of a curleic acid molecule which down regulates expression of a neurite growth inhibitor gene (Nacy). The regulates expression of a neurite growth inhibitor good). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a possessing an NCH motif), a G-cleaver (cleaving RNA with an NCH motif), a G-cleaver (cleaving RNA with an NCH motif) a a manberzyme (cleaving RNA with an NCH motif), a clustoners (cleaving RNA with an NCH with an NCH color) in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, it may be contacted with a call to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma (MLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, leukaemia, and inflammatory arthropathy. The NOGO-targetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the contacted may be contacted with a cell to reduce NOGO gene in the call and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more contacted central nervous system (CNS) injury and cereborovascular accident (CVA, stroke), Allzheimer's disease, dementia, multiple sclerosis (ALS), parkinson's disease, ataxia, Huntington's disease, creative disease central response to the modulation of NOGO expression. The present cates which response to the nodo cates of creates which response to the nodo cates of cates with a response of cates of cates of cates which response to the nodo cates of cates of cates which response to the nodo cates of cates which response to the nodo cate
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CHOWRIRA B M.
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  Synthetic.
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Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other; sequence is a zinzyme molecule of the invention

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Gaps
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68.0%; Score 17; DB 4; Length 17; 70.6%; Pred. No. 3.3e+02;
                              0; Indels
                             Mismatches
                              2,
 Query Match 68.0
Best Local Similarity 70.6
Matches 12; Conservative
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8 GCUUGGAUCACACCCUU 24 ||::|||:|||:|||||:: | GCTTGGATCACACCCTT 1

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ABK01430/c

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ABK01430 standard; RNA; 17 BP.
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ABK01430;

12-MAR-2002 (first entry)

Human NOGO Inozyme #700.

Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; mucollar; CD20; neurite growth inhibitor gene; NGG0; hammerhead ribozyme; DNAzyme; incygme; declader; amberzyme; zinzyme; lincygme; declader; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; ataxia; Huntington's disease; centrafeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens Synthetic. WO200159103-A2.

.6-AUG-2001.

09-FEB-2001; 2001WO-US004273.

11-FEB-2000; 2000US-0181797P-28-FEB-2000; 2000US-0185516P-06-MAR-2000; 2000US-0187128P-

RIBO-) RIBOZYME PHARM INC.

MCSWIGGEN J BLATT L. (BLAT/)

CHOWRIRA B M CHOM/ Chowrira BM; Slatt L, Mcswiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 89; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a neutite growth inhibitor gene (NGO). The regulates expression of a neutite growth inhibitor gene (NGO). The capulates expression of a neutite growth inhibitor gene (NGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a C-cleaver (cleaving RNA with a NYN motif) propered in amberzyme (cleaving RNA with an NYN motif) propered (cleaving RNA with an NYN motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic treat lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HTV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphoma, immunocytoma (IMC), small B-cell lymphoma, immunocytoma (IMC), small B-cell lymphoma, immunocytoma (IMC), small a cell cation associated with the level of nucleic acid may be contacted with a cell to reduce NOGO activity of the cull and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more

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therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; mucular; CD20; neurice growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; delegrowth inhibitor gene; NOGO; hammerhead ribozyme; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphomy; leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntingcon's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                                                                                                                    68.0%; Score 17; DB 4; Length 17; 76.5%; Pred. No. 3.3e+02; ative 4; Mismatches 0; Indels
                                                                                                                                                                 Sequence 17 BP; 4 A; 5 C; 3 G; 0 T; 5 U; 0 Other;
                                                                                                                             sequence is an inozyme of the invention
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                                                                                                                                                                                                                                                                              3 GGAUAGCUUGGAUCACA 19
                                                                                                                                                                                                                                                                                                                                                                                                           ABK02029 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                17 GGATAGCTTGGATCACA 1
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                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOGO Zinzyme #351.
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CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-607195/69.
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLATT L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK02029;
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                                                                                                                                                                                                                                            Matches
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The invention relates to a nucleic acid molecule which down regulates

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Complete and the mendolytic nucleic acid cleaving a an Kwa Maccule Complexing an NCD mocife), a closaving RNA with a NCH mocife), a closaving RNA with an NCH mocife), a closaving RNA with an NCH mocife), a closaving RNA with an NCH mocife), a closaving RNA with a NCH mocife), a closaving RNA with a NCH mocife), a closaving RNA with a CCD closaving RNA of CD20 in the presence of a divalent cation that is preferably MG^2/+.

Complete close in the presence of a divalent cation that is preferably MG^2/+.

Complete close in the presence of a divalent cation that is preferably MG^2/+.

Complete close in particular, the CD20 targetting nucleic acid may be used to the rapies. In particular, the CD20 targetting nucleic acid may be used to creat lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic lenkaemia, HIV (human immunodeficiency virus) associated NHL, lymphocytic lenkaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MC), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma (MC), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MC), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma (MC) immunocytoma (IMC), small B-cell lymphocytic lymphoma, indiced acid is used to cleave RNA of the NOGO gene in the cull and treat a patient having a condition associated with the level of CO presence of a divalent cation that is preferably MG^2+. Furthermore, the therapies In particular, the NOGO-targetting nucleic acid may be used to create central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic baterial sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic baterial sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic baterial sclerosis (MS), chemotherapy-induced neurop
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expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  states which respond to the modulation of NOGO expression. The present
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68.0%; Score 17; DB 4; Length 17;
Best Local Similarity 70.6%; Pred. No. 3.3e+02;
Matches 12; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 5 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is a zinzyme molecule of the invention
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ID ABK01429 standard; RNA; 17 BP
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Matches
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cegulates expression of a neurite growth inhibitor gene (NGOD). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a nRNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) property and NCH motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA contracted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level coff CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic lymphoma, lawphoma immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC) small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, lymphoma, immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC) small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHC, wantle cation that is preferably MG'2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NGGO activity of the cargetic may be contacted with a cell to reduce NGGO activity of the NGGO. The treatment may further comprise the use of one or more theraphes. In particular, the NGGO-targetting nucleic acid may be used to theraphes. In particular, the NGGO-targetting nucleic acid may be used to the central network system (CNS) injury and cerebroorabcular accident
                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemcherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present
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                                                                                                                                                                                                                                                                       Chowrira BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system injury.
                         11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
                                                     28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.
                                                                                                                                   RIBOZYME PHARM INC.
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CHOWRIRA B M.
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 68.0%; Score 17; DB 4; Length 17; 76.5%; Pred. No. 3.3e+02;
Score 17; L. ... Pred. No. 3.3e+02;
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                       13; Conservative
            Local Similarity
 Query Match
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GATAGCTTGGATCACAC 1

Human NOGO DNAzyme #196.

ABK02284 standard; RNA; 17 BP 12-MAR-2002 (first entry) ABK02284; RESULT 7
ABK02284/c
ID ABK022
XX
AC ABK022
XX
XX
DT 12-MAR
DK Human

cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; NDAzyme; inozyme; growth inhibitor gene; NOG0; hammerhead ribozyme; B-cell lymphoma; non-Hodgkin; alymphoma; NHL; lymphocytic leukaemia; Human immunocytoma; non-Hodgkin; alymphoma; NHL; lymphocytic leukaemia; MCL; immunocytoma; NHC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; ceneotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

Homo sapiens. Synthetic.

WO200159103-A2.

16-AUG-2001

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

(RIBO-) RIBOZYME PHARM INC. BLATT L. MCSWIGGEN J. BLAT/)

CHOWRIRA B M (MCSW/) CHOM/) Chowrira BM; Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20.gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemla, and central nervous system injury.

Claim 88; Page 115; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NDGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a divalent cation that is preferably MG² +. Furthermore, it may be contacted with a call to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-flokin's lymphoma (MLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG² +. Furthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO gene in the call and treat a patient having a condition associated with the level of the cell and treat a patient having a condition associated with the level of the reatment may further comprise the use of one or more contral nervous system (CNG) injury and cereborovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, and/or bisease, created verther adisease, central nervous system (CNG) injury and cereborovascular accident central nervous system (CNG) injury and cereborovascular disease ataxia, Huntington's disease, central disease, central disease, ataxia, Huntington's disease, central disease, ataxia, Huntington's disease, ataxia, Hun

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polymerase beta, which is a specific representation of DNA polymerase beta in oesophagus cancer. The protein coded by it has fully lost the DNA repair activity of DNA polymerase beta. It can be used for early diagnosis and gene therapy of esophagus cancer. This sequence represents a human DNA polymerase beta associated oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                  present invention discloses a cDNA sequence of human repair gene DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA inhibition, dsRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; ds.
                                                                                                                                                                                                                                                                                                                                              Human DNA polymerase beta mutant gene and its corresponding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 66.4%; Score 16.6; DB 10; Length 58; Local Similarity 52.2%; Pred. No. 6.1e+02; nes 12; Conservative 7; Mismatches 4; Indels
            Human, repair gene; DNA polymerase beta; oesophagus cancer;
DNA repair activity; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human EGFR inhibitor dsRNA sense strand SEQ ID NO 172.
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26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                         24-AUG-2001; 2001CN-00128374.
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                                                                                                                                                                                                                                                                             Zhao Q;
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                                                                                                                                                                                                                                           (UYZH-) UNIV ZHENGZHOU
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                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a cDNA sequence of human repair gene DNA polymerase beta, which is a specific representation of DNA polymerase beta in esophagus cancer. The protein coded by it has fully lost the DNA repair activity of DNA polymerase beta. It can be used for early diagnosis and gene therapy of esophagus cancer. The present sequence is a DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    human repair gene DNA polymerase beta; gene therapy; esophagus cancer;
                                                                                                      Gaps
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                                                                  Length 17;
                                                                68.0%; Score 17; DB 4; Length 17; 76.5%; Pred. No. 3.3e+02; rative 4; Mismatches 0; Indels
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                                Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
sequence is a DNAzyme molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 13; 18pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                  DNA sequence of the invention #6
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                                                                                                                                      7 AGCUUGGAUCACACCCU 23
                                                                                                                                                          17 AGCTTGGATCACACCCT 1
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ADF73036 standard; cDNA; 58
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                                                                                                                                                                                                                                                                                                                               12-FEB-2004 (first entry)
                                                    Query Match
Best Local Similarity 76.37
These 13; Conservative
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nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao G, Zhao Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD28188 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYZH-) UNIV ZHENGZHOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-240398/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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Best Local S
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ADP73036/C

ADP730

ACD28188/c
ID ACD281
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RESULT 9

Matches

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                                                                                                     The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nuclectides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a dsRNA molecule related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA inhibition; daRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; ds.
               Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the target and having an overhang.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the target and having an overhang.
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                                                                                                                                                                                                                                                                                                                                                           65.6%; Score 16.4; DB 6; Length 22; 77.8%; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human EGFR inhibitor deRNA antisense strand SEQ ID NO 173.
                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 6 A; 6 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hadwiger
                                                                             Claim 13; Page 40; 203pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rost S,
                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGAUAGCUUGGAUCACAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAGCTTGGATCACAC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV78289 standard; RNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-2001; 2001DB-01000586.
26-OCT-2001; 2001DB-01055280.
29-NOV-2001; 2001DB-01058411.
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                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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The invention relates to inhibiting expression of a target gene (I) in scell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1

Claim 13; Page 40; 203pp; German.

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has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        human; cytostatic; immunomodulator; neuroprotective; nootropic; anorectic; antidiabetic; antimidrobial; antilipaemic; gene therapy; vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease; obesity; diabetes; infectious disease; metabolic syndrome X;
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                                                                                                                                                       Length 24;
                                                                                                                                                                                    1; Indels
                                                                                                                             Sequence 24 BP; 5 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
                                                                                                                                                       Score 16.4; DB 6;
Pred. No. 6.7e+02;
0; Mismatches 1;
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                                                                                                   a dsRNA molecule related to the invention
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08-JUN-2002; 2002US-02986971P.
08-JUN-2002; 2002US-029800P.
10-JUN-2002; 2002US-02987535P.
11-JUN-2002; 2002US-0387625P.
11-JUN-2002; 2002US-0387625P.
11-JUN-2002; 2002US-0387634P.
11-JUN-2002; 2002US-0387634P.
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06-JUN-2002; 2002US-0386453P
06-JUN-2002; 2002US-0386864P
06-JUN-2002; 2002US-0387016P
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07-JUN-2002; 2002US-0386816P
07-JUN-2002; 2002US-038693IP
07-JUN-2002; 2002US-0386942P
                                                                                                                                                      / Match 65.6%;
Local Similarity 94.4%;
les 17; Conservative
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                                                                                                                                                                                                                           3 GGAUAGCUUGGAUCACAC
                                                                                                                                                                                                                                                                                                              ADH72558 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2004 (first entry)
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dyslipidaemia; ss; probe
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New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                              2002US-0390763P.
2002US-040128P.
2002US-040128P.
2002US-0402156P.
2002US-040238P.
2002US-0402786P.
                                                                                                                                                                                                                                                          2002US-040635P
2002US-0406240P
2002US-0410004P
2002US-0411528P
2002US-0414801P
2002US-0414801P
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2002US-0403459P.
2002US-0403531P.
2002US-0403532P.
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09-0CT-2002; 2002US-041746FP.
23-0CT-2002; 2002US-041746F9.
28-0CT-2002; 2002US-0422156P.
31-0CT-2002; 2002US-0422690P.
                                                                    2002US-0389884P.
2002US-0390006P.
2002US-0390209P.
                                   2002US-0389144P.
                                                             2002US-0389742P.
                                                                                                                                                            2002US-0402816P.
2002US-0402821P.
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2002US-0406317P.
2002US-0403617P.
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2002US-0414954P.
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                                                                     18-JUN-2002;
19-JUN-2002;
19-JUN-2002;
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17 - JUN - 2002)
06 - AUG - 2002)
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26-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhong H;
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Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangolli EA, Gerlact VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
Maclachlan T, Malyankar UW, Mezick AJ, Millet I, Mishra VS;
Addigaru M, Petturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
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The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidabetic, antimicrobial, and antilipaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising Disclosure; SEQ ID NO 1454; 1880pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                      Query Match 64.8%; Score 16.2; DB 12; Length 26; Best Local Similarity 71.4%; Pred. No. 8.4e+02; Matches 15; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                    Sequence 26 BP; 7 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                   CUGGAUAGCUUGGAUCACACC 21
                                                                                                                                                                                                                                                                                                                                                         CTGGACATCTTGGAACACACC 21
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOGO Zinzyme #350.
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MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-607195/69.
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(MCSW/)
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ABK02028/c
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGO). The nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a nucleic acids an NCH motif), a G-cleaver (cleaving RNA with an NRY motif) propersessing an NCH motif), a G-cleaver (cleaving RNA with an NGN with a NGN motif) propersessing an NCH motif), a G-cleaver (cleaving RNA with an NGN with a call to reduce CD20 acivity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more corrected. The presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of fone or more therapies. In particular, the CD20 targetting nucleic acid may be used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the current lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma (MCC) treatening and insection that is preferably MG<sup>2</sup>+. Furthermore, the creatment may further comprise the use of one or more coll and treat a patient having a condition associated with the level of theraphies. In particular, disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lat
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splice variant, transcriptome, oligonucleotide library, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 6 A; 3 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is a zinzyme molecule of the invention
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02-MAY-2001; 2001US-0287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-257383/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN32813;
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Gaps

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messenger RNAs that populate a Genub-transcriptome, where the Genub-
transcriptome comprises messenger RNAs transcriptome, where the Genub-
transcriptome comprises messenger RNAs transcribed from multiple
transcriptom units that populate a genome. The library comprises several
oligonucleotides, each capable of hybridising selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
quantitatively characterising the corresponding transcriptome, and in
transcriptomes. The libraries may also be used as specialised mini
libraries to detect transcripts of a sub-transcriptome under a particular
biological or pathological state, and so allowing the detection of tissue
and pathology-specific genes such as those genes only expressed in
specific tissue under a specific pathological condition; to detect
developmental specific genes, and to detect RNA transcripts and splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                 New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABNS9589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                             The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, epidermal growth factor receptor; hyperproliferative disease;
Herl, antisense; prophylaxis; psoriasis; phosphorothioate backbone;
tumour; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%; Score 15.8; DB 6; Length 60; 68.4%; Pred. No. 1.5e+03; live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60 BP; 14 A; 13 C; 16 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Her-1 antisense oligonucleotide ISIS #122133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "2'methoxyethyl nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Phosphorothioate backbone"
                                                                                                                     Example 1; SEQ ID NO 5561; 47pp; English.
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/mod_base= m5c
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                                                                            specific genes.
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The invention relates to an antisense oligonucleotide targetted to a nucleic acid molecule encoding human epidermal growth factor receptor (Herl) to inhibit its expression. The antisense compounds are useful for treating diseases or conditions associated with Her-1 such as hyperproliferative diseases especially cancer (lung, ovarian, colon or prostrate cancer) and psoriasis. They are also useful as research reagents, dismostics, therapeutics, kits and prophylactically e.g. to prevent or delay tumour formation. The present sequence is an antisense oligonucleotide targetted to human Her-1
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antisense oligonucleotide that specifically hybridizes with and inhibits nucleic acid encoding epidermal growth factor receptor, useful for treating hyperproliferative disease such as cancer or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.6%; Score 15.4; DB 6; Length 20; 76.5%; Pred. No. 1.9e+03; Ative 3; Mismatches 1; Indels
                                                                          note = "2'methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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Best Local Similarity 76.5
Matches 13; Conservative
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                                               *tag=
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Gaps

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Search completed: July 30, 2005, 15:45:00 Job time : 309.77 secs

1123017A0

us-09-544-776-3.szlm60.rst

Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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AQ072941

BP(2)2154 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from Both 5' and 3' ends of P element, genomic survey sequence.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/clone lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
/melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
insertion strains is described in Rorth P, Szabo K, Bailey
A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
                                                                      ALT77445 ALT77445
CC458457 SALK 1189
CR247136 FOrward a
AR205057 2M0021P24
AV962471 AV962471
N63645 Zal6f12.61
BF036425 60460458
CG669098 AC0059 Sa
BH856117 SALK 0833
H69956 YU72210.61
                                                                                                                                                                                                                                                                                                                                                                             AZ783926 ZM0026002
CD917506 G08.105J
AZ42376 1M0203G22
AU105134 AU105134
BJ000348 BZ000348
CN92292 000411AEL
CN933071 ZF001-P00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 42)
Liao,G.-C., Rehm,B.J. and Rubin,G.M.
Insertion site preferences of the P transposable element
                                                                                                                                                                                                                                                                                                                                                         CG774043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
20202638
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Berkeley Drosophila Genome Project
University of California, Berkeley
University of California, Berkeley
Ess. 5106439947
Email: gerry@fruitfly, berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence recovery method was inverse PCR.
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                                                                                                                                                              AZ782057
AV962471
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BH856117
BH856117
AZ783926
CG774043
AZ783926
CD917506
AZ783769
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CC458457
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CB353071
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AA277710 mv78h05.r

AZ395181 1M0159M03

AA676294 ad37d06.s

AL763703 Arabidops

BG538454 602567160

AL762995 Arabidops

AL97835 uc40e02.y

A141879 tc01h12.x

BH901304 SALK 0743

AA188179 ms30b04.r

AL765094 Arabidops
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Rosso, M.G., Li,Y., Strizhov, N. and Weisshaar, B.

Direct Submission

L Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Suchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At1g48930.

Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated thtp://www.mpiz-koeln.mpg.dGABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 bp DNA linear GSS 01-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-143G03-012977, genomic survey sequence.
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                   genetics in brosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                            57.6%; Score 14.4; DB 8; Length 42;
45.8%; Pred. No. 5e+04;
tive 7; Mismatches 6; Indels
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/clone="GK-143G03-012977"
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/strain="Columbia 0"
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Best Local Similarity
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/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
/note="PCR was performed on DNA from Alante T-DNA from
plants (TI) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ317154
1M0035G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic close UUGC1M0035G16 R, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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/clone_11b="Mouse 10kb plasmid UNGCNM lbrary"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
'clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                             ch 56.8%; Score 14.2; DB 9; Length 46; I Similarity 73.7%; Pred. No. 6.3e+04; 14; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                       T-DNA derived sequences were removed."
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Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: G column: 16
Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0035G16"
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High quality sequence stop: 60.
Location/Qualifiers
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Fax: 801 585 7177
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/note="PCR was performed on DNA from Arabidopsis thaliana plants" PCR was performed on DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA from tragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                           /db_xref="taxon:3702"
/clone="GK-274F03-015094"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     'strain="Columbia 0"
                                                                                                   /ecotype="Col-0"
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 [91]4732114 [91]47123104.], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X1.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                      56.8%; Score 14.2; DB 8; Length 60; 68.4%; Pred. No. 6.5e+04; ive 3; Mismatches 3; Indels
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/clone lib="ASLV-vector integration sites in human 293T-TVA cells"

Lonce="Human 293T cells expressing the subgroup A avain retrovirus receptor (293T-TVA) were infected with an ASLV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the ASLV cDNA. Junctions between integrated ASLV proviruses and cellular DNA were cloned and sequenced."
                                                                                                                                                                                                                                                                                                                                                            CL528471
ASV13H02.fwd ASLV-vector integration sites in human 293T-TVA cells
Homo sapiens genomic clone ASV13H02.fwd, genomic survey sequence.
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1 (bases 1 to 55)
Mitchell.R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H., Berry, C.C., Ecker, J.R. and Bushman, F.
Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target Site Preferences
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Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
ch 56.0%; Score 14; DB 9; Length 45; I Similarity 54.5%; Pred. No. 7.8e+04; 12; Conservative 5; Mismatches 5; Indels

    .55
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="ASV13H02.fwd"
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/organism="Arabidopsis thaliana"

/mol_type="genomic_DNA"

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Arabidopsis thaliana T-DNA flanking sequence GK-265D06-014998,
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/clone="GK-265D06-014998"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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Pred. No. 1.2e+05;
5; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics 19 (11), 1441-1442 (2003)
                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
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/strain="Columbia 0"
CTGAGTAGCTGGGACCACAGGCATG 36
                                                                                                                                                       genomic survey sequence.
                                                                                                                                                                                             AL942366.1 GI:24398964
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Best Local Similarity 55.0%;
Matches 11; Conservative
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58 bp mRNA linear EST 10-JUN-1998 ol67£12.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534703 3, similar to TR:Q99622 Q99622 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE AA918654
BH908280 SALK 046972.17.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_046972.17.10.x, genomic
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,B. Bcker,J.R.
Shinn,P., Zammerman, Information for Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="SALK 046972.17.10.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Mipublished (2001)
Mipublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/organism="Arabidopsis_thaliana"
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/ecotype="Col-0"
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Email: ddunn@genetics.utah.edu
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Fax: 801 585 7177
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                                                                                                          Timor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E, Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE617639 36 bp mRNA linear BST 20-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DHIOB"
/clone lib="NCI CGAP Kid3"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. WRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 58)
                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 519 Std Brror: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534703"
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M. Fatima Bonaldo.
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Homo sapiens
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                     Mus musculus Endazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 36)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Dasmid inserts
Unpublished (2000)
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2M0059H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic CODE UUGC2M0059H15 F, genomic survey sequence.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAM9557 row: c column: 24
High quality sequence start: 18
High quality sequence stop: 36.
Location/Qualifiers
1. 36
/organism="Homo sapiens"
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Plate: 0059 row: H column: 15
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0059H15"
/sex="Male"
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Location/Qualifiers
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Gaps

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/dev stages="adult"
//dev stages="adult"
//dev stages="adult"
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//clone=lib==1007 - RescueMu Grid H"
//clone=lib==1007 - RescueMu (engineered from
//clone=lib==1007 - RescueMu (engineered from
//clone=lib==1007 - RescueMu (engineered from
//clone=lib==1007 - RescueMu is a 4.9 kb, modified maize Mu transposon
//clone=lib==1007 - RescueMu is a 4.9 kb, modified maize Mu transposon
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1007088F11.IEL_y1 1007 - RescueMu Grid H Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007088 column: 32
Class: transposon-tagged.
Location/Qualifiers
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// organism="Zea mays"
/mol type="genomic DNA"
/cullivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
                                                                                                                                   3; Indels
                                                        Score 13.2; DB 8;
Pred. No. 1.7e+05;
5; Mismatches 3;
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                                                                   52.8%;
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                                                                                                                                   10; Conservative
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                     Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH814737 25 bp DNA linear GSS 02-MAY-2002 SALK 066889 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_066889, genomic survey sequence.
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids; ll; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Sahinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Arabidopsis Genome
Ombublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fex: 858 558 6379
musculus C57BL/6J (male) was obtained from the Jackson
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Arabidopsis thaliana
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/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 52.28
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AA207740

59 bp mRNA linear EST 12-MAR-1997
mw78b105.r1 GuayWoodford Beier mouse kidney day 7 Mus musculus cDNA
clone IWAGE:661209 5' similar to gb:X13661 Mouse mRNA for
elongation factor 1-alpha (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 59)
Marram, Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:661209"
/tissue_type="kidney"
/dev etage="juvenile"
/lab_host="Solk" (kanamycin resistant)"
/lab_host="Solk" (kanamycin resistant)"
/clone lib="GuayWoodford Beier mouse kidney day 7"
/note="Organ: kidney; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Cligo dT. Average insert size: 1.0 kb; Uni ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Library provided
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1M0159M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0159M03 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.linl.gov) for further information. MGI:407057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marking M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.8%; Score 13.2; DB 1; Length 59; 66.7%; Pred. No. 1.9e+05; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Seg primer: -28mil revl ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                            AZ771156
51 bp DNA linear GSS 16-FEB-2001
1M0573C12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0573C12 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                      Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musin Li (basea 1 to 51)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Moderhausern, A. and Mright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Mright, D., Weiss, R.
                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606

Pax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0573 row: C column: 12

Seg primer: CGTTCTAAAACGACGCCAGT

Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0573C12"
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Location/Qualifiers
                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                           AZ771156
AZ771156.1 GI:12893112
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FEATURES

GSS 03-OCT-2000

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RESULT 14

Query Match

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Matches

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Gaps

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil-4732114 [gb]-AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                             Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
RM: 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Pwrified genomic DNA from M.musculus G5PBL/6J (male) was obtained from the Jackson
   1 (bases 1 to 59)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0159 row: M column: 03
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plaamid ends
High quality sequence stop: 59.
Location/Qualifiers
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/organism="Mus musculus"
/orl type="genomic DNA"
/strain="c57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0159M03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male'
REFERENCE
AUTHORS
                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                 TITLE
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Score 13.2; DB 8; Length 59;
Pred. No. 1.9e+05;
4; Mismatches 3; Indels
 ch 52.8%;
l Similarity 61.1%;
11; Conservative
Query Match
Best Local Similarity
Matches 11; Conservat
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Search completed: July 30, 2005, 18:20:42 Job time : 2432.72 secs

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Sequence 100, App
Sequence 100, App
Sequence 12, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 75584, A
Sequence 39, Appl
Sequence 39, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 124476,
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41, Appl
1184, Ap
66, Appl
177, App
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13, Appl
                                                                       July 30, 2005, 15:05:52; Search time 87.8378 Seconds (without alignments) 465.710 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-676-610B-38
US-09-985-162-100
US-09-910-1053-100
US-09-10-63-100
US-09-186-737B-12
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US-08-324-243-25
US-08-532-390-25
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                     - nucleic search, using sw model
                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                 US-09-544-776-3
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 60
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76462, A
4, Appli
6, Appli
21, Appl
134, Appl
17, Appl
297, App
                                                   9, Appli
168, App
10858, A
28, Appl
16, Appl
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Sequence 38, Application US/09676610B

SENERAL INFORMATION:
SENERAL INFORMATION:
The Particant: C. Frank Bennett
APPLICANT: Susan M. Freier
TILLS OF INVENTION: OLICONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182

SEQ ID NO 38

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Patent No. 6057156

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: PACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: LOS Angeles
STATE: California
COUNTRY: U.S.A.
                   PCT - USSS-11511-25
PCT - USSS-11511-25
PCT - USSS-11965A-9
US-08-983-605-1088
US-08-276-968A-28
US-09-274-752D-16
US-09-396-1966-76462
US-09-439-813-6
US-09-439-813-6
US-09-439-813-6
US-09-439-813-6
US-09-791-105B-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGAUAGCUUGGAUCACA 19
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ORGANISM: Artificial Sequence
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Gaps

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GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
APPLICANT: Young, Yasen K.Y.
TITLE OF INVENTION: Primers and Probes for Detection of
TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.6%; Score 14.4; DB 4; Length 17; Best Local Similarity 75.0%; Pred. No. 1.3e+03; Matches 12; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Elbopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
                  FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
APPLICATION NUMBER: 60/036,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Siam Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08240547; Patent No. 5527669
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MOLECULE TYPE: DNA (genomic)

US-08-240-547-3
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-09-401-063-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Nutl
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-240-547-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 100, Application US/09401063
; Sequence 100, Application US/09401063
; GENERAL INFORMATION:
APPLICANT: Akhtar: Saghir
APPLICANT: ROSWiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLBIC ACID TREATMENT
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
ADDRESSEE: LYON & LYON
               COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TBM Compatible
COMPUTER: TBM Compatible
COMPUTER: TBM COMPATIBLE
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION DATE: 60/036,476
FILING DATE: 31 January 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 230/107
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRANE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15" Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURREMT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AUAGCUUGGAUCACAC 20
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY: linear
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                                                                                     Score 14; DB 4; Length 40;
Pred. No. 2.3e+03;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 2; Length 57;
Pred. No. 2.4e+03;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Primer used for CYP2A6 genotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07605
FILING DATE: 16-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 75584, Application US/09396196G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFFECT 5.1
CURRENT APPLICATION NUMBER: US/08/750,703
                                                                                                                                                                                                                                          34 TGGATGGGTTGGATCAACACT 13
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REGISTRATION NUMBER: 36,434
REPERRICE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPRAS: (212) 758-4800
TELEPRAS: (212) 75-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: oligonucleotide
                                                                                     Query Match 56.0%;
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.0%;
Best Local Similarity 59.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: C.C. ZIP: 10154-0053
COMPUTER READABLE FORM:
TYPE: Floppy disk
; OTHER INFORMATION: GENOMIC US-10-071-485-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: F4 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
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US-09-396-196G-75584/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      US-08-750-703-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-750-703-10
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

### APPLICANT: Buyse, Marie-Ange

### APPLICANT: Sablon, Erwin

### TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

### TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

### TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

### CURRENT PILING DATE: 2000-02-14

### PRIOR APPLICATION NUMBER: PCT PP 98/05165

### PRIOR PILING DATE: 1998-06-18

### PRIOR FILING DATE: 1998-06-18

### PRIOR FILING DATE: 1999-06-18

### PRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
TITLE OF INVENTION: SHOCK,
TITLE OF INVENTION: GACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT APPLICATION NUMBER: PC7/8P 98/05165
PRIOR PILING DATE: 109485,737
PRIOR PELING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 12
TEXAMALE: PATENTIN VERSION 3.0
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   Pred. No. 1.8e+03;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14; DB 3; I
Pred. No. 2.3e+03;
6; Mismatches 5;
                                                                                                                                                                                                                                                               US-09-485-737B-12/c
; Sequence 12, Application US/09485737B
; Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 UGGAUAGCUUGGAUCACACCCU 23
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Patent No. 6830752
                                                                                                                         AGCTTAGATCACTCCCCTG 22
                                                                                        7 AGCUUGGAUCACACCCUUG 25
   Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.0%;
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: GENOMIC US-09-485-737B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-10-071-485-12/c
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Gaps
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US-09-205-860-53/c
; Sequence 53, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILLE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT PILING DATE: 1998-12-04
; NUMBER 0F SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.4%; Score 13.6; DB 3; Length 56; 55.0%; Pred. No. 3.8e+03; Live 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: El PR FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US/08/513/1993
FILING DATE: 11-MRAR-1993
FILING DATE: 11-MRAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                         STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Antisense Oligonucleotide US-09-205-860-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CUGGAUAGCUUGGAUCACAC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618 REPERENCE/DOCKET NUMBER: EDATELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-513-968-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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US-09-396-196G-94761

Sequence 94761
Sequence 94761
Sequence 94761
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOSTWARE: FRSECE for Windows Version 4.0
                                                                                                                APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-513-968-39
'Sequence 39, Application US/08513968
'Patent No. 6114143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 UAGCUUGGAUCACACCCUUG 25
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MAKIZUMI, Kelichi
SHIOSAKI, Kouichi
OSATOMI, Kiyoshi
KIMACHI, Kazuhiko
HIGUCHI, Hirofumi
                                                        GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: mus musculus US-09-396-196G-75584
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US-09-396-196G-94761
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APPLICANT: BDA, Yas,
APPLICANT: MAEDA, H
APPLICANT: SHIOSAKI
APPLICANT: SHOSAKI
APPLICANT: KIMACHI,
APPLICANT: HIGUCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 94761
LENGTH: 25
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Query Match 53.6%; Score 13.4; DB 5; Length 40; Best Local Similarity 52.2%; Pred. No. 4.5e+03; Matches 12; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00909
FILING DATE: 19910208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 990008.408PC
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sledziewski, Andrzej Z.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Protein-Coupled Receptors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application PC/TUS9100909
GENERAL INFORMATION:
APPLICANT: Sledatewski, Andrzej Z.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00909
FILING DATE: 19910208
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: United States
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 3723836
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: United States
ZIP: 98104-7092
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STRANDEDNESS: single
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PCT-US91-00909-10
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-396-1966-124476
; Sequence 124476, Application US/09396196G
; Patent NO. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REPERBNCE: 310.1.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR PILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: EastSEQ for Windows Version 4.0
; SEQ ID NO 124476
; LENGTH: 25
                                                                                                                                                                             US-09-396-196G-21284

Sequence 23284, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: APFLICANT: David Lockhart

APPLICANT: APPLICANT: David Lockhart

APPLICANT: APPLICANT: OB THE STANDAN MACK

TILLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT PRILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1998-09-17

WHORER OF SEQ ID NOS: 127806

SOFTWARE: PASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
PCT-US91-00909-10
; Sequence 10, Application PC/TUS9100909
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                                1 CUGGAUAGCUUGGAU 15
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16 CTGGATAACTTGGAT 2
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Best Local Similarity 73.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Mus musculus
US-09-396-196G-23284
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Gaps

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ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REPERENCE/DOCKET NUMBER: 990008.408PC

FELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 206-622-4900

TELEFAX: 206-632-6031

TELEFAX: 206-632-6031

TELEFAX: 206-632-6031

TELEFAX: 3723836

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPLOGGY: linear

MOLECULE TYPE: cDNA

PCT-US91-00909-13

Query Match

S3.6%; Score 13.4; DB 5; Length 43;

Best Local Similarity 52.2%; Pred. No. 4.5e+03;

Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Search completed: July 30, 2005, 18:25:12 Job time: 89.8378 secs

28 TGAGTAGCAACGATCATACCCTT 6

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Scoring table:

Searched:

Minimum DB e Maximum DB e

Database

Perfect score:

Sequence:

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OM nucleic

Run on:

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PAT 08-DEC-1995
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1 (bases 1 to 42)

Barry, T.G., Gannon, B.X. and Powell, R.

Barry, T.G., Gannon, B.X. and Powell, R.

Batry, Thomas Gerard, Gannon, Bernard Francis Kavier; BIORESEARCH

BRITY, Thomas Gerard; Gannon, Bernard Francis Kavier; BIORESEARCH

IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas

Gerard; Gannon, Bernard Francis Kavier; BIORESEARCH IRELAND;

Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas

Gannon, Bernard Francis Kavier; BIORESEARCH IRELAND;

Gannon, Bernard Francis Kavier; BOLAS (trading as BioResearch

Ireland) - The Irish Science and Technology Agency; Powell,

Richard; UNIVERSITY COLLEGE GALWAY
                                     AX241495 Sequence
BD073932 RTD recep
AX09786 Sequence
AX365647 Sequence
AX365647 Sequence
BD222069 SH2 domai
AX179726 Sequence
AX179726 Sequence
AX1718032 Nicotiana
BD15864 A method
CQ547443 Sequence
ES9733 Method for
AX646405 Sequence
ES9733 Method for
AR646105 Sequence
ES9733 Method for
AR654005 Sequence
CQ543976 Sequence
CQ543976 Sequence
CQ543946 Sequence
CQ543946 Sequence
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Pred. No. 4.6e+03;

    42
    Acganism="synthetic construct"
/mol_type="unassigned DNA"
    Ab _xref="taxon:32630"

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DNA probe (A.salmonicida) from
A32068
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AJ719032
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AR011196
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I17834
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66.7%;
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synthetic construct
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A32288 DNA probe (
A32049 DNA probe (
A32067 DNA probe (
                                                                                                                                                    July 30, 2005, 12:54:37; Search time 718.243 Seconds (without alignments) 1686.588 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            nucleic search, using sw model
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AR365637
AR365666
BD134588
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AX539243
AR254609
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A32288
A32049
A32067
CQ544937
AX215126
AR365650
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Match Length
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PAT 08-DEC-1995

A32288 42 bp DNA linear DNA probe (A.salmonica) from patent BP0395292. A32288

E59732 BD012596 BX088624

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Other sequences; artificial sequences.

1 (bases 1 to 59)

Barry, T.G., Gannon, B.X. and Powell, R.

Generation of specific probes for target nucleotide sequences

Patent: EP 0395292-A 42 31-0CT-1990;

Barry, Thomas Gerard, Gannon, Bernard Francis Xavier; BIORESEARCH

IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas

Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;

Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas

Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch

Ireland) - The Irish Schence and Technology Agency; Powell,

Richard; UNIVERSITY COLLEGE GALWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice
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64.8%; Score 16.2; DB 6;
Best Local Similarity 57.1%; Pred. No. 4.7e+03;
Matches 12; Conservative 6; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Patent: WO 0210449-A 14572 07-FEB-2002;
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CQ544937
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Sequence 568 from Patent WO0159103.
AX215126
AX215126.1 GI:15525169

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Location/Qualifiers
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                     A32067.1 GI:1249522
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synthetic construct
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Best Local Similarity 66.7
Matches 14; Conservative
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AX215126/c
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KEYWORDS
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JOURNAL
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(bases 1 to 59)

Barry, T.G., Gannon, B.X. and Powell, R.

Generation of specific probes for target nucleotide sequences Patent: EP 0395292-A 24 31-0CT-1990;

Barry, Thomas Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard; Cannard Francis Cannon, Bernard Francis Cannon, Bernard Kavier; BOLAS (trading as BioResearch Ireland) - The Irish Science and Technology Agency; Powell, Richard; UNIVERSITY COLLEGE GALWAY
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                                                                                 cother sequences; artificial sequences.

1 (bases 1 to 42)

Barry, T.G., Gannon, B.X. and Powell, R.

Generation of specific probes for target nucleotide sequences

Patent: EP 0195292-A 49 31-OCT-1990;

Barry, Thomas Gerard, Gannon, Bernard Francis Xavier; BIORESEARCH

Barry, Thomas Gerard, Gannon, Bernard Francis Xavier; BIORESEARCH

FIRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas

Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;

Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;

Gannon, Bernard Francis Xavier; EDLAS (trading as BioResearch

Ireland) - The Irish Science and Technology Agency; Powell,

Richard; UNIVERSITY COLLEGE GALWAY
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DNA probe (A.hydrophila) from patent EP0395292.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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CTGCAGGATTCCAGACATGTC 8
  A32288.1 GI:1249529
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Matches 14; Conservative
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A32067/c
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PAT 03-SEP-2003
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Shah,J., Buharin,A. and Lane,D.J.
Nucleic acid probes for the detection of Pneumocystis carinii
Patent: US 5519127-A 4 21-MAY-1996;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 39)
Shah, J., Buharin, A. and Lane, D.J.
Nucleic acid probes for the detection of Pneumocystis carinil Patent: US 5519127-A 33 21-MAY-1996;
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Pred. No. 9.3e+03;
6; Mismatches 4; Indels
                                          Score 15.6; DB 6; Length 33;
Pred. No. 9.3e+03;
6; Mismatches 4; Indels
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Pred. No. 9.3e+03;
6; Mismatches 4;
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Sequence 33 from patent US 5519127.
AR365666
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Sequence 4 from patent US 5519127.
AR365637
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/mol_type="genomic DNA"
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/wol_type="genomic DNA"
 /mol_type="genomic DNA"
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Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local Similarity 54.5%;
Matches 12; Conservative
                                           Query Match 62.4%;
Best Local Similarity 54.5%;
Matches 12; Conservative
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Unclassified.
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AR365666
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                                                     Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 568 16-AUG-2001;
RIBOSYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknow...
Unclassified.
1 (bases 1 to 33)
Shah,J., Buharin,A. and Lane,D.J.
Nucleic acid probes for the detection of Pneumocystis carinil
Patent: US 5519127-A 17 21-MAY-1996;
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Unclassified.
1 (bases 1 to 33)
1 (bases 1 to 33)
Shah,J., Buharin,A. and Lane,D.J.
Nucleic acid probes for the detection of Pneumocystis carinii
Patent: US 519127-A 36 21-MAY-1996;
Location/Qualifiers
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                                                                                                                                                                                                                                                                     64.0%; Score 16; DB 6; Length 17; 75.0%; Pred. No. 5.6e+03;
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                                                                                                                                                                             /organism="synthetic construct"
/mol type="unassigned RNA"
/mol type="taxon:32630"
/nore="Nucleic Acid"
                             other sequences; artificial sequences.
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/organism="unknown"
/wol_type="genomic DNA"
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AR365650.1 GI:34429562
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synthetic construct
synthetic construct
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AR365669
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AR365650
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PAT 23-NOV-2002
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
Patent: WO 0210449-A 6447 07-FBB-2002;
                                                                                                                                                                                                                                    Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 015103-A 1442 16-AUG-2001;
RIBOZYME FHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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                                                                                  AX216000
Sequence 1442 from Patent WO0159103.

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Location/Qualifiers
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17 ATTCCAGATATGCCC 3
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synthetic construct
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AX216000/c
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AX539243
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CQ536812
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CIZNI5/09,CO7K14/705,C12N5/10,C12N7/00,C12P21/02,C12Q1/02, PC
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Patent: WO 0159103-A 567 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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 Dioxin receptor gene and utilization thereof.
                                                                                                                                                  Dioxin receptor gene and utilization thereof
Patent: JP 2002045188-A 5 12-FEB-2002;
SUMITOWO CHEMICAL CO LTD
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(C12N5/00,C12R1:93)
Designed oligonucleotide primer for PCR
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Best Local Similarity 70.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 4; Mismatches 1;
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Seguence 567 from Patent WO0159103.
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Prinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
Patent: WO 02059142-A 30 01-AUG-2002;
Epidauros Biotechnologie AG (DE)
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/organia="synthetic construct"
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/db_xref="taxon:32630"
                                                                              synthetic construct
synthetic construct
other sequences; artificial sequences.
Sequence 30 from Patent W002059142. AX539243 GI:25272457
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Search completed: July 30, 2005, 16:20:40 Job time: 720.243 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 60

Total number of hits satisfying chosen parameters:

4390206 segs, 2959870667 residues

Searched:

Gapop 10.0 , Gapext 1.0

4316768

genesequ1990s:* genesequ2000s:* genesequ2001as:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* N Geneseq 16Dec04:* geneseqn2001bs:* geneseqn1980s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2004as:* geneseqn2004bs:*

geneseqn2003cs:* geneseqn2003ds:*

Aac64408 Human Nog Abn41824 Human spl Abt60568 Human NoG Ad164316 Human sin Adr77241 Human apo Adr77241 Human apo Adr76955 Human apo Adr76955 Human apo Adr80188 Human apo Add10823 Preumocys
Ad42447 Probe 148
Ab140079 Phosphoen
Ab154676 Cricetulu
Abk00567 Human NOG
Abk1442 Human NOG
Abh313699 Human spll
Ab866695 Human mul Aat14558 Cytotacti Adn76060 C japonic Adf41788 Bacillus Description SUMMARIES ADR80185 ADR76955 ADR76330 AAQ10823 AAAT4247 ABL44079 ABL54676 ABK00567 ABK00442 ABK01442 ABK01442 ABK01442 AAT14558 ADN76060 ADF41788 ADR 79899 AAC64408 ABN41824 ADL64316 ADR77241 ABK00568 8 Query Match Length 0444 Score 15.8 115.8 115.8 115.8 115.6 115.6 115.6 14.8 14.8 14.6 14.6 Result Š 0000000

Aaa62887 Forward P	Aaq66143 DNA-polym	Adn11426 FLJ14528	Aaf92390 T7 clone	Aan92390 Sequence	Adj63889 Plant lip	Adl64169 Human sin	Aaz88270 Sec B nuc	Abz00890 Human leu	Adr35716 Human nic	Adr35715 Human nic	Adr35713 Human nic	Adr35714 Human nic	Abn34410 Human spl		Abl58226 Virulence		Aad03304 Reverse p	Aax28212 Tumour an	Adc82787 DNA seque	Acc43414 PCR prime		Aat42445 Probe 149	Ab140078 Phosphoen	Abk52807 Human pro
AAA62887	AAQ66143	ADN11426	AAF92390	AAN92390	ADJ63889	ADL64169	AAZ88270	ABZ00890	ADR35716	ADR35715	ADR35713	ADR35714	ABN34410	ABK02644	ABL58226	AAX25095	AAD03304	AAX28212	ADC82787	ACC43414	AAQ10833	AAT42445	ABL40078	ABK52807
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14.6	14.6	14.6	14.4	14.4	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14	14	14	14	14	14	14	14	14	14	14
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ALIGNMENTS

Human, Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; antisense; Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4. BP. AAC64408 standard; RNA; 25 (first entry) phosphorothioate; ss. Homo sapiens 08-FEB-2001 AAC64408; RESULT 1 AAC64408

/*tag= a
/*note= "phosphorothioate linkages" Location/Qualifiers modified_base Key

2000WO-US009383 99US-0128372P. (CHIR) CHIRON CORP. WO200060083-A1 07-APR-2000; 08-APR-1999; 21-JUN-1999; 12-OCT-2000.

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

Williams LT;

Halenbeck R,

Wei D,

WPI; 2000-665007/64.

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or
                                                                The present invention describes a human stress-phosphorylated endoplasmic
                                                                                   reticulum protein, designated Noge B. Nogo B has cytostatic activity and cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for and distinguishing Nogo B polypeptides are useful for and distinguishing Nogo B polypeptides polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligonucleotide from the present invention
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   Claim 25; Page 32; 68pp; English
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ABN41824 standard; DNA; 60 BP
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02-MAY-2001; 2001US-0287724P.
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quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathology specific genes such as those genes only expressed in specific tissue under a specific pathology specific of a transcriptome of a patient specific pathology specific pathology specific pathology septemental specific genes; and to detect RNA transcripts and splice developmental specific genes; and to detect RNA transcripts and splice developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABNS9589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; crebbroprotective; antiparkinsonian; muscular; CD20; neuroprotective; antiparkinsonian; muscular; CD20; neuroprotective; antiparkinsonian; DNAzyme; inozyme; inozyme; inozyme; inozyme; deleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; MCL; immunofeticiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; MC; immunocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; central acident; GYA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.2; DB 6; Length 60;
Pred. No. 9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60 BP; 12 A; 13 C; 13 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
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28-FEB-2000; 2000US-0185516P.
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06-MAR-2000; 2000US-0187128P.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1
Matches 12; Conservative
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regulates expression of a color and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acid molecule which down contacts acids may be enzymatic nucleic acid e.g. a ribozyme or a manbezyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaving caid cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more conformation in particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic cleukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (MCL), small B-cell lymphocytic lymphoma, cleukaemia, and inflammatory arthropathy. The NOGO gene in the comparism of the contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce NOGO activity of the contaction and particular and particular and for a condition associated with the level of the contaction and compared to requese the order of the contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce NOGO activity of the contaction of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity of the NOGO activity o
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growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                          invention relates to a nucleic acid molecule which down regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is a hammerhead ribozyme of the invention
                                                                                                              Claim 88; Page 75; 200pp; English
                                           central nervous system injury.
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Gaps ö Score 16; DB 4; Length 17; Pred. No. 9.4e+02; 1; Mismatches 0; Indels Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other; 64.0%; Sco. 75.0%; Pred. No. 9... Local Similarity 75.0 Query Match Best Loca Matches

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16 GATTCCAGATATGCCC 1 GAUUCCAGAUAUGCCC 10 8 셤

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ADL64316 standard; DNA; 41 BP 20-MAY-2004 (first entry) ADL64316; ADL64316/c RESULT 4

Human single nucleotide polymorphism (SNP) #239.

se; human; single nucleotide polymorphism; SNP;

Cl S subcomponent protein; ClS; alanyl aminopeptidase protein; ANPEP;
meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
tissue kallikrein protein; KKL; aminopeptidase P protein; XPN-PEPL;
tissue kallikrein protein; KKL; aminopeptidase P protein; MEPLB;
soluble guanylate cyclase l alpha-2 subunit protein; GUCY1A2; haplotype;
angloedema; angloedema-like disorder; paternity testing;
cardiovascular diseases; angina pectoris; hypertension; heart failure;
myocardial infarction; aneurysm; stroke; embolism; thrombosis;
coronary artery disease; arteriosclerosis; hypertension;
haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
asthma; chronic obstructive pulmonary disease; cough reflex; allergy; cancer; ANPEP

Homo sapiens

human gene encoding a protein, such as the C1, S subcomponent protein (CC human gene encoding a protein, such as the C1, S subcomponent protein (human gene encoding a protein, such as the C1, S subcomponent protein (CC (C1S), the alanyl aminopeptidase protein (XPN-PED.), the aminopeptidase protein (XPN-PED.), the aminopeptidase p-like protein (XPN-PED.), the aminopeptidase p-like protein (XPN-PED.), the muncleic acid comprises at least one polymorphic position. (CUCYLA2). The nucleic acid comprises at least one polymorphic position. The colding the allelses reference alleles and alternate alleles of the single nuclectide polymorphicms, listed in the specification. The polymorphic position resides in a (non)coding position within the genomic sequence of the gene. The polymorphic position residing in a coding position resides within the untranalated region or an intronic region of position resides within the untranalated region or an intronic region of position resides within the untranalated region or an intronic region of the gene. Comprises using the nucleic acids above further comprises using the haplotypes to identify an individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the haplotypes to identify an individual for the presence of angloedema-like disorder. The nucleic acids and polypeptides can be used in diagnosing, cusqual in phenotype correlations, paternity testing, medicine and genetic analysis. The nucleic acids and polypeptides can be used in diagnosing, perventing or treating cordinates, myoractial infarction, aneurysm, creve, embolism, thrombosis, coronary artery disease or arterioscleroals, hypersensitivity reactions and probes are pectoris, hypertension, heart failure, myocardial infarction, aneurysm, seption, inflammatory diseases, inflammatory diseases, inflammatory diseases, inflammatory diseases, inflammatory diseases, inflammatory diseases, inflammato Gaps . Perrone M, Powell JR, Ramanathan CS, Swanson B; New nucleic acid comprising a single nucleotide polymorphism at a specific location, useful in paternity testing, genetic analysis or diagnosing, preventing or treating cardiovascular diseases e.g. ö 64.0%; Score 16; DB 12; Length 41; 58.3%; Pred. No. 1.1e+03; ive 5; Mismatches 5; Indels Sequence 41 BP; 9 A; 5 C; 13 G; 14 T; 0 U; 0 Other; Claim 3; SEQ ID NO 239; 376pp; English. 2 AACUUCAGGAUUCCAGAUAUGCCC 25 34 AACTACAGGATTACACATCTGTCC 11 angioedema or angina pectoris. 03-JUN-2003; 2003US-00453827. 03-JUN-2002; 2002US-0384980P. Query Match
Best Local Similarity 58.3.
Best Local 14; Conservative Edmonds M, Hui L, Perr Tsuchihashi Z, Zerba K; POWELL J R. RAMANATHAN C S. SWANSON B. TSUCHIHASHI Z. WPI; 2004-180052/17. EDMONDS M. PERRONE M. of the invention. ZERBA K. US2004033582-A1 19-FEB-2004. (RAMA/) F (SWAN/) S (TSUC/) 1 (ZERB/) Z EDMO/) PERR/) POWE/) ઠે g

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ADR79899 standard; DNA; 19 BP RESULT 5 ADR79899/c A

(first entry)

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The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have cone or more asymmetrical 2'-O alkyl modifications, the antisense cone or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (MI) apoB-100 clevels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and cintroducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (C) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (C) the subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted control disregulation of lipid metabolism. The clevels of cholesterol imbalance, dyslipidaemias, hypercholestorolaemia, statin-resistant hypercholesterolaemia, statin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                    antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV; MAX interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; ALDS; apolipoprotein B; apoB; ss.
                                                                                                    Human apolipoprotein B (ApoB) oligonucleotide seqid 4395.
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13-MAR-2003; 2003US-0454962P.

13-MAR-2003; 2003US-0455050P.

14-APR-2003; 2003US-0462894P.

17-APR-2003; 2003US-046565P.

25-APR-2003; 2003US-046565P.

25-APR-2003; 2003US-0465602P.
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11-AUG-2003; 2003US-0494597P.
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                                                           16-DEC-2004
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                     ADR 79899;
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2003US-0518453P

2003US-0452682P

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disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocereballar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; anticonvulsant; notropic; muscula; anti-HIV; cytostatic; anticonvulsant; notropic; muscula; anti-HIV; cholesterence; iRNh; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose-metabolism-related disorder; disease; cancer; breast cancer; colon cancer; lung cancer; neurological disease; Huntington disease; spinocerebellar ataxia; viral disease; ALDS; apolipoprotein B; apoB; ss.
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57.9%; Pred. No. 1.2e+03;
tive 6; Mismatches 2;
                                                                                                                                                                                                                                                                                            Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
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2003US-0518453P.
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2003US-0454265P
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07-NOV-2003;
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17-APR-2003;
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                                        The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical phosphorothicate modifications come or more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described and the antisense sequence targets a human gene sequence. Also described care: a pharmaceutical preparation comprising (I); reducing (II); involves selecting a sequence with activity and levels or glucose-6-phosphatase levels in a subject; producing (I); involves selecting a sequence with activity and citroducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and adevice that can be dispense or administer a composition comprising (I) is activity; a kit comprising (I) and instruction for its use; and adevice that can be dispense or administer a composition comprising (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. Coherwise unwanted expression of apoB-100, elevated or otherwise unwanted correction of apoB-100, elevated or otherwise unwanted correction of apos-100, elevated or otherwise unwanted corrections and or dispense or type-2 diabetes (CAD), coronary heart of dispense (CAD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism.

Condisease (CAD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism.

Condisease (CAD) and sease as mentioned above, cancer (e.g. breast, colon or columpace and disease as mentioned above, cancer (e.g. breast, colon or columpace and disease as mentioned elevels. Also antisease (e.g., Albabetes or type-2 diabetes. (I) is useful for corrections or columpace and administration or columpace and administration or columpace and administration o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulaant; nootropic; muscula; anti-HIV; RNA interference; iRNA; antisense technology; lipid metabolism; cholesterol imbalance; dyslipidaemia hypercholesterolaemia; coronary artery disease; CAD; coronary heart disease; CHD; atheroselerosis; hepatic glucose production; glucose-metabolism-related disorder; diabetes; cancer; breast cancer; olon cancer; lung cancer; alway cancer; hug cancer; hug cancer; hug cancer; nursi disease; Runtington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8; DB 13; Length 19;
Pred. No. 1.2e+03;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human apolipoprotein B (ApoB) oligonucleotide segid 4682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used to control ApoB gene expression.
                Example 5; SEQ ID NO 1726; 378pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ACUUCAGGAUUCCAGAUAU 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 63.2%;
Local Similarity 57.9%;
les 11; Conservative 6
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12-MAR-2003; 2003US-0454265P.
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the invention describes a raw interference (irray, again, 14) computating a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 19-0 alkyl modifications, the antisense sequence and more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100 comporting or glucose-6-phosphatase levels in a subject; producing (I); thyolves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted expression of apoB-100, elevated or otherwise unwanted chose from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant consary heart classes (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-craface dispense or craface (CHD) and atherosclerosis. (I) is administered or subject to inhibit hepatic glucose production or for treating glucose-etabolism craface dispense (E.) intentioned above, cancer (e.g., huntington disease or subject to subject to be proceedeal at easily or virtal disease (e.g., huntington disease or construction or for treating the disease or huncor in the subject of the subject is subjected to a subject to be subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject to be a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a RNA interference (iRNA) agent (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.2e+03;
6; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
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ID ADR76955 standard; DNA; 19 BP.
25-APR-2003; 2003US-0465665F
25-APR-2003; 2003US-0465802P
09-MAY-2003; 2003US-0465802P
08-AUG-2003; 2003US-0493986F
11-AUG-2003; 2003US-0494597P
                                                                                                                                                                                                                                           2003US-0506341P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manoharan M, Bumcrot D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALMY-) ALMYLAM PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-677362/66.
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                                                                                                                                                                                                                                                                                                     09-OCT-2003;
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07-NOV-2003; 2003US-0518453P

2003US-0510318P

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coronary artery disease; CAD; coronary heart disease; CHD; atherosclerosis; hepatic glucose production; glucose_metabolism_related disorder; diabetes; cancer; breast cancer; colon cancer; lung cancer; leurological disease; Huntington disease; spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
                                                                                                    antidiabetic;
                                                                                              antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidi
cytostatic; anticonvulaant; nootropic; muscula; anti-HIV;
RNA interference; isRNA; antisense technology; lipid metabolism;
cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
Human apolipoprotein B (ApoB) oligonucleotide seqid 1440.
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Homo sapiens

MO2004080406-A2.

23-SEP-2004

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13-MAR-2003; 2003US-0454962P.

13-MAR-2003; 2003US-0455050P.

14-APR-2003; 2003US-0462894P.

17-APR-2003; 2003US-0463772P.

25-APR-2003; 2003US-0465665P.

25-APR-2003; 2003US-0465602P.

09-MAY-2003; 2003US-046902P.

08-AUG-2003; 2003US-046912P.
                                                                                                                                                                                                                                                                                   11-AUG-2003; 2003US-0494597P
                                                                                                                                                                                                                                                                                                      2003US-0506341P
2003US-0510246P
                                            2003US-0452682P
2003US-0454265P
08-MAR-2004; 2004WO-US007070
                                                                                                                                                                                                                                                                                                         26-SEP-2003;
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(ALNY-) ALNYLAM PHARM

Bumcrot Manoharan M,

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WPI; 2004-677362/66.

Interference RNA agent useful for treating dyslipidemias, coronary disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.

artery

Example 5; SEQ ID NO 1440; 378pp; English.

The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2-0 alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothicate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (MI) apobl-100 levels or glucose-6-phosphatase levels in a subject; producing (I); etabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apobl-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apobl-100, elevated or otherwise unwanted levels or dispense or administer a composition of lipid metabolism. The levels of cholesterol, and/or disregulation of lipid metabolism. The childen and application of lipid metabolism. The childen and application of lipid metabolism. The childen and application of lipid metabolism. dysilpidaemias, hypercholestorolaemia, statin-resistant hypercholesterolaemia, coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or

non-modified nucleic acid residues which are useful as primer in nucleic acid extension and amplification reactions and as capture probe in single mucleotide polymorphism (SNP) assays. Multiple primers are used in multiplex PCR. The invention is useful in diagnostic purposes, as probes in the purification, isolation and detection of pathogenic organisms such as virus, bacteria or fungi, as generic tools for purification, raplification and detection of nucleic acids from groups of related species such as for instance rRNA from gram-positive or gram negative bacteria, fungi, mammalian cells. It is also useful as an aptamer in molecular diagnostic e.g. in RNA mediated catalytic processes, in specific binding of antibiocics, drugs, amino acids, peptides, structural proteins, protein receptors, saccharides, enzymes, polygaccharides, biological cofactors, nucleic acids, or triphosphates or

invention relates to chimeric oligonucleotide containing modified and

Example 1; Page 9; 12pp; English.

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lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric oligonucleotide useful as primer in nucleic acid extension and amplification reactions and as capture probe in single nucleotide polymorphism assays, has non-modified and modified nucleic acid residues.
                                                                                                                                                                                                                                                                                                     Single nucleotide polymorphism; SNP; antisense therapy; viral infection;
                                                                                                       Gaps
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                                                                                Length 19;
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                                                                               Query Match
63.2%; Score 15.8; DB 13;
Best Local Similarity 57.9%; Pred. No. 1.2e+03;
Matches 11; Conservative 6; Mismatches 2;
                                                         Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Apo B3500 DNA amplifying reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jakobsen MH, Kongsbak L, Pfundheller H;
                                                                                                                              3 ACUUCAGGAUUCCAGAUAU 21
                                                                                                                                           19 ACTTCAAGGTTCCAGATAT 1
                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                            AAD48330 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                    PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2002.
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Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

in the separation of enantiomers from racemic mixtures by stereospecific binding. It is also used in antisense therapy for treating diseases e.g. viral infection. The present sequence is a PCR primer used for amplifying Apo B3500 DNA. This sequence is used in the exemplification of the

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11-JUN-2001; 2001WO-CN000950.
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                                                                                                                                                                                          STAD ) AMOCO CORP
                                                                                                                21-JAN-1992;
                                          US5519127-A.
                                                                             21-MAY-1996
     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This oligonucleotide has a sequence specific for a region of the rDNA of Pneumocystis carini, the causative agent of pneumonia. It can be used as a probe in hybridisation assays to detect P. carinii in clinical samples. This probe detects human but not most non-human P.carinii isolates. See also AAQ10820-22 and AAQ10824-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; pneumocystis carinii; 18S rRNA; human; mammal; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid fragment - capable of hybridising to r RNA or r DNA o pneumocystis carinii, useful as probes for detection of P carinii.
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     Length 20;
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Pred. No. 1.6e+03;
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                                        Indels
                                                                                                                                                                                                                                                                                                                      Pneumocystis carinii 18S rRNA-targetted probe, 1485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;
 Score 15.8; DB 10;
Pred. No. 1.2e+03;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Hybridisation assay; pneumonia; AIDS; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe 1485 for P. carinii 18S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 11; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
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                                                                                               1 ACTTCAAGGTTCCAGATAT 19
                                                                           3 ACTUCAGGATUCCAGAUAU 21
                                                                                                                                                                                                         BP
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   63.2%;
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Local Similarity 54.5%;
les 12; Conservative
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AAT42447 standard; DNA; 34
                                                                                                                                                                                                       AAQ10823 standard; DNA; 34
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                                                                                                                                                                                                                                                                                 09-MAY-1991 (first entry)
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                                        11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shah JS, Buharin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-073563/10,
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                  RESULT 10
AAQ10823/C
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AAT42443-T42456 represent probes for human Pneumocystis carinii (Pc) 1882 TRNA. Pc infects humans and most mammalian hosts, but rarely cause illness in normal individuals. However, in certain conditions of each contain individuals. However, in certain conditions of the immunodeficiency, Pc does give rise to life threatening pneumonia. This sequence hybridises to the 188 rRNA at positions 641-652, and is capable of hybridisation to human Pc. These probes can be used as a probe set for a Pc assay. The 1485 (this sequence), 1487 (see AAT42452) and 1159 (see AAT42448) probes are reactive with all human Pc isolates. The probes 1485 and 1487 hybridise to rRNA and rDNA of human Pc, but not to other fungi or bacteria. The 1485 and 1487 probes can therefore be used to detect Pc in clinical samples. The rest of these probe sequences are reactive mainly with ferret Pc and non-human strains of Pc. By using these probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; phosphoenolpyruvate-dependent sugar phosphotransferase 12; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mainly with ferret Pc and non-human strains of Pc. By using these probe sequences, a more sensitive, accurate and rapid diagnosis can be performed, with reduced expense, in comparison to current technology. RRNA is present in the cell at high concentration, and is not likely to undergo lateral transfer. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid probes specific for human Pneumocystis carinii - provide sensitive, accurate and rapid diagnosis of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CUUCAGGAUUCCAGAUAUGCCC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Col 13-14; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      079/c
ABL40079 standard; DNA; 41 BP.
92US-00826657.
                                                                                                                                                                                                                                                                                                        Shah J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2002 (first entry)
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Gaps

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Length 20; Indels

Mao Y,

and

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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. aribozyme or a DNAzyme) an NOH motif), a G-cleaving RNA with a NYM motif) pr an amberzyme (cleaving RNA with an NOK triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleaving NNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg<sup>-2</sup>+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; Jymphoma; leukaemia; Human immunodeficiency virus; HIV associated NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; inmunocytoma; IMC; immune thrombocytopaemia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease, ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
61.6%; Score 15.4; DB 6;
70.6%; Pred. No. 1.9e+03;
ive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOGO Hammerhead Ribozyme #567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chowrira BM;
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                                                                                                      1 CAACUUCAGGAUUCCAG 17
                                                                                                                                                                                                                                                                                       ВР.
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                       ABK00567 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                             Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHOWRIRA B M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-607195/69.
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MCSWIGGEN J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                       ABK00567;
       Query Match
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                                                                                                                                                                                                                                     RESULT 14
ABK00567/c
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                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human phosphoenolpyruvate-dependent sugar phosphotransferase 12 (1). (1) has cytostatic, haemostatic, virucide, immunomodulatory and antiinflammatory activities. The polynucleotide (1) encoding (1) can be used in gene therapy. (1) and (II) can be used in the diagnosis and treatment of malignant tumour, haemopathy, human mimunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The present sequence represents a probe for (I), which is used in an example from the present invention
                                                                                                                                                                                                           Phosphoenolpyruvate-dependent sugar phosphotransferase 12 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a Cricetulus griseus dioxin receptor gene (ABLS4672) encoding a dioxin receptor (ABLS686) or having an amino acid sequence at least 95 % homologous. The dioxin receptor gene can be used for measuring dioxin-like substances. The present sequence is that of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A dioxin receptor gene useful for measuring dioxin-like substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.4%; Score 15.6; DB 6; Length 41; 59.1%; Pred. No. 1.7e+03; ive 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41 BP; 8 A; 11 C; 14 G; 8 T; 0 U; 0 Other;
                                                          (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
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                                                                                                                                                                                                                                                                                                                                          Example 6; Page 16; 33pp; Chinese.
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Query Match

Matches

8 셤 Seguence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

RESULT 13
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treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
Hodgkin's lymphoma (HRL), bulky low-grade or follicular non-
Hodgkin's lymphoma (HRL), bulky low-grade or follicular NHL, lymphocytic
leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
immune thrombocytopaemia, and inflammatory arthropathy. The NOGO-
targetting nucleic acid is used to cleave RNA of the NOGO gene in the
presence of a divalent cation that is preferably MG'2+. Furthermore, the
uncleic acid may be contacted with a cell to reduce NOGO activity of the
cell and treat a patient having a condition associated with the level of
NOGO. The treatment may further comprise the use of one or more
therapies. In particular, the NOGO-targetting nucleic acid may be used to
treat central nervous system (CNS) injury and cerebrovascular accident
(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
disease, muscular dystrophy, and/or other neurodegenerative disease
states which respond to the modulation of NOGO expression. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
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60.0%; Score 15; DB 4; Length 17; 73.3%; Pred. No. 2.9e+03; Live 4; Mismatches 0; Indels 11 AUUCCAGAUAUGCCC 25 17 ATTCCAGATATGCCC 3 11; Conservative Best Local Similarity Query Match Matches

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Gaps . 0

Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; incyme; G-cleaver; amberzyme; zinzyme; loukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntingcon's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Chowrira BM;

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 89; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGOD). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving RNA with a NRN motif), a G-cleaver (cleaving RNA with a NRN motif) propersessing an NCH motif), a G-cleaver (cleaving RNA with a NCH with a NCH with a NCH with a NCH with a NCH with a CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg² +. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic Lymphoma, leukaemia, HJV (human immunodeficiency virus) associated wHL, mantle-cell lymphoma (MCL), immunocytoma (MCL), small B-cell lymphocytic lymphoma, crimine thrombocytopaenia, and inflammatory arthropathy. The NOGO targetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg² 2+. Furthermore, the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more concleic acid may be contacted with a cell to reduce NOGO gene in the cell and treat a patient having a condition associated with the level of treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzhaimer's disease, dementia, multiple sclerosis (ALS), chemocherapy-induced neuropathy, and/or other neurodegenerative disease central respond to the modular disease, created spatial sclerosis (ALS), and sease, ataxia, Huntington's disease, created search to the present contacted to the present ce sequence is an inozyme of the invention

Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Gaps .. 0 Score 15; DB 4; Length 17; Pred. No. 2.9e+03; 4; Mismatches 0; Indels 4; Mismatches 60.0%; 73.3%; 11; Conservative Query Match Best Local Similarity

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10 GAUUCCAGAUAUGCC 24 15 GATTCCAGATATGCC 1 .. 셤 Search completed: July 30, 2005, 15:45:02 Job time : 309.77 secs

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CK415880 CK415880 R7173 yy88£02.r1 CL529721 HVV58E3.y BE320905 NP028B03R C20879 HVMGS000494 BH855668 SALK 0848 AA780094 &£6569.8 CK403886 Arabidops CR403886 Arabidops CR403886 Proward 8 AZ54580 1M0080013 AZ94759 2M0249F02 AL768749 Arabidops AU107193 AU104145 AU107193 AU104145 AU107193 AU104145 AU107193 AU104145 AU107193 AU104145 AU107193 AU104145 AZ555018 1M0248E05 BK659005 Arabidops

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Scoring table:

Searched:

Database

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 53)
Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 bp mRNA linear EST 25-APR-; cDNA library Mus musculus cDNA clone
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/mol type="mRNA"
/db xref="taxon:10090"
/clone="BED001210"
/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
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BED0012210 3', mRNA sequence.
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BX530982 A
AW156165 B
BX532084 P
BX532497 A
AIG25497 A
AIG25480 CR110498 E
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gaps

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AQ072891 40 bp DNA linear GSS 23-AUG-2000 EP(2)2087-5prime Drosophila melanogaster EP line Drosophila

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE

REPERENCE

JOURNAL MEDLINE

PUBMED

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nhigeanger ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Fbrojects/T_brucei/.
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2M0130E20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0130E20 R, genomic survey sequence.
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G. Blrect Submission Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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59.2%; Score 14.8; DB 9;
Best Local Similarity 61.1%; Pred. No. 3.8e+04;
Matches 11; Conservative 5; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="163c01"
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Insert Length: 10000 Std Error: (
Plate: 0130 row: E column: 20
Seq primer: CACACAGGAAACGCTATGACC
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University of Utah Genome Center
University of Utah
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High quality sequence stop: 51.
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Fax: 801 585 7177
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the 8 base target
             melanogaster genomic Sequence recovered from 5' end of P element,
                                                                                                                                                  Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 40)

Liao,G.-C., Rehm,B.J. and Rubin,G.M.

Insertion site preferences of the P transposable element in Drosophila melanogaster

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence recovery method was inverse PCR.
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                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwalot (gilly 4732114 [gb] AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weissbaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
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Arabidopsis thaliana T-DNA flanking sequence GK-488F11-019586,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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Pred. No. 9.6e+04;
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Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
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                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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organism="Mus musculus"
                                                            /db_xref="taxon:10090"
/clone="UUGC2M0130E20"
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CTTAAGGACTCCAGGTATATCC
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54.5%;
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Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B..

Birect Submission

Loudited (31-Mar. 2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-Mar. 2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-Mar. 2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5905120.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

Location/Qualifiers
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Welsshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
Elanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Makaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="GK-488F11-019586"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Weisshaar, B.
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22755829
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/strain="Columbia 0"
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BX532135.1 GI:31409265
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Best Local Similarity 55.01
Matches 11; Conservative
(bases 1 to 45)
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organism="Homo sapiens"
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Af596320. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project (GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1992 Std Error: 0.00
Seq primer: -400P from Gibco
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wj94c07.x1 NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2410476 3',
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  High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                4 (bases 1 to 47)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission
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44 AGCTTGAGGATCCCACATAT 25
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Homo sapiens
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Strichov, N., Li,Y., Rosso, M.G. and Weisshaar, B.

Strichov, N., Li,Y., Rosso, M.G. and Weisshaar, B.

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Strichov, N., Li,Y., Rosso, M.G. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5963120.

Details on the protocols used for generation of the sequence are described in References 1-3. The sequence are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI-'wmw.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers
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Arabidopsis thaliana T-DNA flanking sequence GK-471A05-019883,
                                                                                                                                                                                                                                /clone lib="NCI_CGAP_Lyml2"
/note="Corgan: lymph node; Vector: pCMV-SPORT6; Site_1:
/note="Corgan: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
/mol_type="mkNA"
/db_xref="taxon:9606"
/clone="IMAGE:2410476"
/tissue_type="lymphoma, follicular mixed small and large
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Hajh-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.4%; Score 13.6; DB 1; Length 50; 60.0%; Pred. No. 1.5e+05; ive 4; Mismatches 4; Indels
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XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction Kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Arabidopsis thaliana T-DNA flanking sequence GK-487A04-019572,
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Weisshaar, B.
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Weisshaar,B.
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Pred. No. 1.5e+05;
5; Mismatches 4; Indels
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Arabidopsis thaliana
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il Similarity 55.0%;
11; Conservative
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                                                                                                                                                                                                                                                     /ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAcifs (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theishing, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
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se20603.yl Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-1758 5', mRNA sequence.
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/tissue type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
/clone lib="Gm-c1015"
/note="Vector: pBluescript II XR; Site_1: BcoRI; Site_2:
                                                                                                                                                                                   /clone="GK-471A05-019883"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Public Soybean EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                          organism="Arabidopsis thaliana"
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/mol_type="mRNA"
/cultivar="Williams 82"
                                                                                /mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                     xref="taxon:3702"
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for

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/lab_host="DH10B"
/clone llb="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDN and Decentification of Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                 /ecctype="Col-0"
/note="For was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAcifi (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                              /mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon 3702"
/clone="GK-491H10-019646"
/clone="GK-491H10-019646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA_Library_Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.4%; Score 13.6; DB 9; Length 59; 55.0%; Pred. No. 1.5e+05;
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                                                                                                                                     organism="Arabidopsis thaliana"
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/db xref="taxon:9606"
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56 AGCTTGAGGATCCCACATAT 37
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Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.

Direct Submitssion
Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5905120.

Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
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                                                                                                                                                                                                                                               /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequence to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                         /clone="GK-487A04-019572"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.4%; Score 13.6; DB 9; Length 59; 55.0%; Pred. No. 1.5e+05; ive 5; Mismatches 4; Indels
                                                                  organism="Arabidopsis thaliana"
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22755829
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Arabidopsis thaliana
                                                                                           /mol_type="genomic_DNA"
/strain="Columbia 0"
                                                                                                                                                   xref="taxon:3702"
           location/Qualifiers
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56 AGCTTGAGGATCCCACATAT 37
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                                                                                                                                                                                                                              ecotype="Col-0"
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BX532497.1 GI:31409627
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CR110498 51 bp DNA linear GSS 05-JUL-2004 Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN410j21, genomic survey sequence.
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
                                                                                                 GSS; genome survey sequence, MICER.
Mus musculus (house mouse)
Mus musculus (hotazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                          1. .51
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN410j21"
/clone_lib="MHPN"
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                                                               CR110498
CR110498.1 GI:49857913
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BM360861.1 GI:18101607
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Matches 13; Conserv
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                                                         Anderson, S. I., Finlayson, H. A. and Archibald, A. L.
Anderson, S. I., Finlayson, H. A. and Archibald, A. L.
Develogment of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roslin Institute
Roslin, Midlochian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector: plueScriptII(SK+) R. Sitel: BcoRI
R. Site2: Not1 5' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8 - cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.
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AJ558580 KN277 Sus scrofa cDNA clone C0005213_H23, mRNA sequence.
AJ658580
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                       - oligo(dT)
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was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I
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Pred. No. 1.6e+05;
5; Mismatches 1; Indels
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/mol_type="mRNA"
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/clone="C0005213 H23"
/tissue_type="embryo"
/clone_lib="KN277"
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Matches 14; Conserv
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SOURCE
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AJ658580
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AUTHORS
TITLE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 60)

S. Chen, Y. and Zhang, Y.Z.

Expressed sequence tags from a subtracted cDNA library of human rectum adenocarcinoma

I. Chin. J. Lymphology Oncol. 2 (2), 9-14 (2002)

Contact: Yao Chen

Life Science College of Sichuan University and the department of anatomy of basic and legal medical institute of west china medical center of Sichuan University

Chengdu, Sichuan University

Chengdu, Sichuan, P.O.box 610041, P.R.CHINA

Tel: 86 028 5501261

Email: **amxfMc23.net
Insert Length: 60 Std Brror: 0.00.
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                                                                                                                                                                                                                                                                                         60 bp mRNA linear EST 09-APR. e cDNA subtractive library of human rectum adenocarcinoma Homo BA360861
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/clone lib="cDNA subtractive library of human rectum
adenocarcinoma"
                                                                    Gaps
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0
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ch 53.6%; Score 13.4; DB 9;
1 Similarity 56.5%; Pred. No. 1.8e+05;
13; Conservative 4; Mismatches 6;
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RESULT 14 CR110498/c

8

Query Match 53.6%; Score 13.4; DB 4; Length 60; Best Local Similarity 52.2%; Pred. No. 1.96+05; Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps

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2 AACUUCAGAUUCCAGAUAUGCC 24 ||||:||||||:|| 22 AACCTCAGGATTCTCCCTCTGCC 44

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Search completed: July 30, 2005, 18:20:53 Job time : 2439.72 secs 1855, Ap 1855, Ap 1856, Ap 1857, Ap 1858, Ap 16064, A

12, Appl 12, Appl

5, Appli 5, Appli 2846, Ap 845, Ap 42375, A 93769, A

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5519127-17
; PACENT NO. 5519127
; PACENT NO. 5519127
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 18/07/826,657
; FILING DATE: 21-73N-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
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TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF THE OF SEQUENCES: 57
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/826,657
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 392,679
FILING DATE: 11-AUG-1989
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US-09-827-998-1855
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US-09-396-1966-16064
US-09-396-1966-1568
US-08-793-958-12
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Sequence 22, Appl
Sequence 64379, A
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Sequence 15817, A
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465.710 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5519127-36
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
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seq length: 60
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5519127-4/c
;Patent No. 5519127
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; Patent No. 5519127
; Patent No. 5519127
; Patent No. 5519127
; Patent No. 5519127
; TILLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF TILLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
FILING DATE: 21-JAN-1992
; RICH APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; RICH APPLICATION NUMBER: 192,679
; PILING DATE: 11-AUG-1989
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5519127-36
Fatent No. 5519127
APPLICANT: SHAH, JYOTSNA; BUHARIN, AMELIA, LANE, DAVID J.
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
FUNDANCYSTIS CARINII
NUMBER OF SEQUENCES: 57
CURRENT APPLICATION DATA:
FILING DATE: 11-JAN-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 11-AUG-1989
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; Patent No. 5519127
APPLICANT: SHAH, JYOTSNA; BUHARIN, AMELIA; LANE, DAVID J.
APPLICANT: SHAH, JYOTSNA; BUHARIN, AMELIA; LANE, DAVID J.
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF; PNEUMOCYSTIS CARINII
CURRENT APPLICATION DAYS:
CURRENT APPLICATION DAYS:
FILING DATE: 21-JAN-1992
PRIOR APPLICATION NUMBER: 392,679
FILING DATE: 11-AUG-1989
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Pred. No. 3.4e+02;
6; Mismatches 4; Indels
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54.5%;
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Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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Best Local Similarity
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APPLICANT: SHAH, JYOTSNA, BUHARIN, AMELIA, LANE, DAVID J.
APPLICANT: SHAH, JYOTSNA, BUHARIN, AMELIA, LANE, DAVID J.
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
PREMOCYSTIS CARRIANS: 57
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/826,657
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 392,679
FILING DATE: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF PREMOCYSTIS CARINII

NUMBER OF SEQUENCES: 57

CURRENT APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/826,657

FILING DATE: 21-JAN-1992

PRIOR APPLICATION NUMBER: 392,679

FILING DATE: 11-AUG-1989
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PAPELICANT: SHAH, JYOTSNA, BUHARIN, AMELIA, LANE, DAVID J.

TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF THE DETECTION OF CURRENT APPLICATION DATA:

PRINGE OF SEQUENCES: 57

CURRENT APPLICATION DATA:

FILING DATE: 21-JAN-1992

PRIOR APPLICATION DATE:

PRIOR AP
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Pred. No. 3.4e+02;
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4 CUUCAGGAUUCCAGAUAUGCCC
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Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local Similarity 81.8*
Matches 18; Conservative
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Gaps

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Indels

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE S:

ADDRESSEE: The SCRIPPS Research Institute, Office of

ADDRESSEE: Patent Counsel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLIG DATE: PCT/US95/11684
FILLIG DATE: 14-SEP-1995
CLASSIFICATION:
  5
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Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 10666 North Torrey Pines Road, TPC 8 CITY: La Jolla STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
IIILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-5EP-1994
ATTORNEY AGENT INFORMATION:
NAME: Logan, April C.
REGISTATION NUMBER: 33,950
REFRERNCE/DOCKET NUMBER: BEC0019P
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64379, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                             5 UUCAGGAUUCCAGAUAUG 22
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14 TTCAGAATTCCAGAAATG 31
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14 TTCAGAATTCCAGAAATG 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
  11; Conservative
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STRANDEDNESS: sing
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US-09-396-196G-64379
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Sequence 22, Application US/08793273C

Retent No. 6482410

GENERAL INFORMATION:

APPLICANT: Crossin, Kathryn L.

APPLICANT: Phillips, Greg

APPLICANT: Pricto, Anne L.

TITLE OF INVENTION: CYTOTACTNI DERIVATIVES THAT STIMULATE ATTACHMENT AND TITLE OF INVENTION: CYTOTACTNI DERIVATIVES OF MAKING SAME

TITLE OF INVENTION: CYTOTACTNI DAY NUMBER: US/08/793,273C

CURRENT APPLICATION NUMBER: US/08/793,273C

CURRENT FILING DATE: 1995-09-14

PRIOR PILING DATE: 1995-09-14

PRIOR FILING DATE: 1996-09-16

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 22

LENGTH: 38

TURENT PILING DATE: 1994-09-16

LENGTH: 38
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                                                                  Score 15.6; DB 6; Length 39;
Pred. No. 3.5e+02;
0; Mismatches 4; Indels
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Pred. No. 8.6e+02;
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                                                                                                                                                                                                                                                                                                            Sequence 88973, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; PILE REFERENCE: 310.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT APPLICATION NUMBER: 60/100,678
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR PRILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PESESEQ for Windows Version 4.0
; SEQ ID NO 88973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.0%; Score 15; DB 4; 18est Local Similarity 56.5%; Pred. No. 6.4e+02; Matches 13; Conservative 5; Mismatches 5
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                                                                Query Match 62.4%;
Best Local Similarity 81.8%;
Matches 18; Conservative (
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ORGANISM: Artificial Sequence
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US-09-396-196G-88973
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Best Local Similarity
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US-09-396-196G-88973
; LENGTH: 39
5519127-33
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US-08-793-273C-22
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US-09-196-118281/C
i Sequence 118281, Application US/09396196G
i Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Mitchael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITILE REFERENCE: 3101.1
CURRENT APPLICATION: Methods of Genetic Analysis
FILE REFERENCE: 1910.1
CURRENT PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FBSESCE OF Windows Version 4.0
SEQ ID NO 118281
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US-09-396-196G-83713/c
; Sequence 83713, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; TILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; RINGR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FESTENCE OF Windows Version 4.0
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64379
LENGTH: 25
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Best Local Similarity 63.2<sup>3</sup>
Matches 12; Conservative
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Best Local Similarity 57.9
Matches 11; Conservative
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; ORGANISM: mus musculus
US-09-396-196G-118281
                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-64379
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CQ538100 Sequence
CQ538479 Sequence
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1533 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="Nucleic Acid"
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Sequence 1534 from Patent WO0159103.
AX216092.1 GI:15526135
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                                                                  July 30, 2005, 12:54:37; Search time 689.514 Seconds (without alignments) 1686.588 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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nogo gene expression
Patent: WO 0159103-A 2081 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
MCSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Patent: WO 0159103-A 2693 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
MCSW199GN, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Patent: WO 0159103-A 1532 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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/mol_type="unassigned"
/note="Nucleic Acid"
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/noFe="Nucleic Acid"
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Sequence 2693 from Patent WO0159103.
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Best Local Similarity 82.4%;
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 015103-A 1774 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                                                              Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 1534 16-AUG-2001;
RIBOZYMS PHRAMACEUTIOLALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/noTe="Nucleic Acid"
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/mol type="unassigned RNA"
/db_xref="taxon:32630"
/nofe="Nucleic Acid"
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Pred. No. 1e+04;
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synthetic construct
other sequences; artificial sequences.
                            other sequences; artificial sequences.
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Sequence 2081 from Patent WO0159103.
AX216639.1 GI:15526700
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Sequence 1774 from Patent WO0159103.
AX216332
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76.5%;
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les 13; Conservative
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/map="7q35-q36"
Fitssue_type="muscle"
/note="isolated from patient with untreated recent onset
juvenile dermatomyositis"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
Patent: WO 0210449-A 6841 07-FEB-2002;
   for Education and Research (CMIER), 2430 N. Halsted, Chicago, 60614, USA
                                                                                                                                                                                                                                                                                                                                                                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 15.4; DB 6; Length 60; 76.5%; Pred. No. 4.6e+04; Live 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                            /codon_start=2
/product="T-cell receptor beta"
/protein_id="AAP3628.1"
/db_xref="GI:7110212"
/translation="VYFCASSSSYRRNQPQHFG"
                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.6; DB 9;
Pred. No. 3.7e+04;
4; Mismatches 4;
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Sequence 6841 from Patent W00210449.
CQ537206.1 GI:41503470
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CQ001884
CQ001884.1 GI:41008516
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                            1. .60
/organism="Homo sapiens"
                                                                                        /mol type="mRNA"
/isolate="patient 133"
/db_xref="taxon:9606"
/chromosome="7"
                                       location/Qualifiers
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Location/Qualifiers
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13 TGCCAGCAGTTCCTCATATAGG 34
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Best Local Similarity 63.6%;
Matches 14; Conservative
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/note="TCRB"
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Homo sapiens
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CQ001884
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CQ537206
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2 (bases 1 to 60)
Pachman,L.M., Liotta,M.R., Lawton,T., Morello,F., Pope,R.M.,
Wu,T.T. and Concannon,P.
Direct Submission
Submitted (01-NOV-1999) Immunology, Children's Memorial Institute
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 60)
Pachman, L. M., Liotta, M.R., Lawton, T., Morello, F., Pope, R.M., Wu, T.T. and Concannon, P.
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Receptor Oligoclonality in Muscle Biopies of DQA1*0501 Caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 2694 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Homo sapiens T-cell receptor beta mRNA, partial cds.
AP200461
                                                                                                                          Query Match 66.7%; Score 16; DB 6; Length 17; Best Local Similarity 81.2%; Pred. No. 3.1e+04; Matches 13; Conservative 3; Mismatches 0; Indels
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1. .17
/organism="synthetic construct"
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/note="Nucleic Acid"
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Best Local Similarity 75.0%; Pred. No. 3.1e+04;
Matches 12; Conservative 4; Mismatches 0;
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/mol_type="unassigned RNA"
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/noTe="Nucleic Acid"
                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
other sequences; artificial sequences.
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Sequence 2694 from Patent W00159103.
AX217252
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AX217252/c
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PAT 16-JAN-2004

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Patent: WO 0159103-A 2082 16-AUG-2001;
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12 TTCACTTGTGGCTCAGATAGG 32
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Best Local Similarity
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 714 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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                                              Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0147944-A 524 05-JUL-2001;
Curagen Corporation (US)
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Sequence 2082 from Patent W00159103.
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Sequence 714 from Patent WO0159103.
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18 TCGTCAGTGCCTCAGACAG 37
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Matches 12; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
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73.3%; Pred. No. 9.1e+04;
tive 4; Mismatches 0; Indels
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Horlick, R.A. and Chelsky, D.
Method for maintenance and selection of episomes
Patent: US 6417002-A 12 09-JUL-2002;
Location/Qualifiers
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60.8%; Score 14.6; DB 6;
Best Local Similarity 61.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 4; Mismatches 4;
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Sequence 12 from patent US 6417002.
AR217875
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Query Match 60.0%; Score 14.4; DB 6; Length 60; Best Local Similarity 58.3%; Pred. No. 1.4e+05; Matches 14; Conservative 4; Mismatches 6; Indels
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/noTe="Primer"
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Sequence 4 from Patent WO2004035787.
CQ809740.1 GI:47115115
                                                                                                                                                                                                                                                                        synthetic construct
synthetic construct
other sequences; artificial sequences.
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Transplantable cell
Patent: WO 2004035787-A 4 29-APR-2004;
F. HOFFWANN-LA ROCHE AG (CH)
Location/Qualifiers
                                                                     1 AUUCCACCAGUGCCUCAGAUAGGA 24
                                                                                       36 ATTCCCTCAGTGCATCAAATGGA 59
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CQB09740
LOCUS
DEFINITION
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Search completed: July 30, 2005, 16:20:41 Job time : 690.514 secs

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July 30, 2005, 12:18:17; Search time 295.459 Seconds (without alignments) 480.857 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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24
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aac64409 Human Nog	Adp17627 Renal cel	Abk02693 Human NOG	Abk01533 Human NOG	Abk01534 Human NOG	Abk02081 Human NOG	Abk01774 Human NOG	Adp17626 Renal cel	Abk01532 Human NOG	Abk02694 Human NOG	Adp48303 Human lym	Aav05323 PCR prime	Abs68889 Human Rec	Abn34093 Human spl	Aal27316 Human SNP	Abk02082 Human NOG	Abk00714 Human NOG	Abz00669 Human leu	Aci32957 Human mic	Aaa29906 Promoter
SUMMARIES	Ü	AAC64409	ADP17627	ABK02693	ABK01533	ABK01534	ABK02081	ABK01774	ADP17626	ABK01532	ABK02694	ADP48303	AAV05323	ABS68889	ABN34093	AAL27316	ABK02082	ABK00714	ABZ00669	ACI32957	AAA29906
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	Query Match	100.0	91.7	70.8	70.8	70.8	70.8	70.8	70.8	66.7	66.7	65.0	65.0	64.2	64.2	63.3	62.5	62.5	62.5	60.8	0.09
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Aaa29903 Promoter	Abz06926 Human leu	Abz06536 Human leu	Adg99916 Kidney di	Abn47833 Human spl	Ado07638 Transgeni	Aat98136 Primer V-	Aax85979 PCR prime	Aax88155 T cell re			Abg01115 Oligonucl			Aah45308 Human Bcl	Aai66468 P53 tumou	-	Adi92963 Thermus s	Adr37349 Human nic	Adr37347 Human nic	Adr37350 Human nic	Adr37348 Human nic	Abn35366 Human spl	Abn32987 Human spl	Aat00607 21-hydrox
AAA29903	ABZ06926	ABZ06536	ADG99916	ABN47833	AD007638	AAT98136	AAX85979	AAX88155	ABQ06198	ABQ06157	ABQ01115	ACI45153	AAA50260	AAH45308	AAI66468	AD192962	AD192963	ADR37349	ADR37347	ADR37350	ADR37348	ABN35366	ABN32987	AAT00607
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0.09	0.09	0.09	0.09	0.09	59.2	59.2	59.2	59.2	59.2	59.2	59.2	59-2	59.2	59.2	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	57.5
14.4	14.4	14.4	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14	14	14	14	14	14	14	14	14	13.8
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ALIGNMENTS

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AAC64409 standard; RNA; 24

RESULT 1 AAC64409 (first entry)

08-FEB-2001 AAC64409;

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists. Human, Nogo B; cell stress response; hyperphosphorylated; brain tumour; stress-phosphorylated endoplasmic reticulum protein; cytostatic; gene therapy; cell growth; cellular stress response; neuron growth; regulator of oxidative stress; inhibitor of neurite outgrowth; axon regeneration; diagnosis; cancer; identification; antisense; phosphorothioate; ss. Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:5. .24 a
 /*tag= a
 /note= "phosphorothioate linkages" Location/Qualifiers Williams LT; 07-APR-2000; 2000WO-US009383. 99US-0128372P. 99US-0140331P. Halenbeck R, WPI; 2000-665007/64. (CHIR) CHIRON CORP. WO200060083-A1 Key modified_base 08-APR-1999; 21-JUN-1999; Homo sapiens 12-OCT-2000. Wei D, X4111X8X1X8X18X6X6X6X1113X8X4X6X8X6X6X6X6X6X

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The present invention describes a human stress-phosphorylated endoplasmic
                                             reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for add distinguishing Nogo B polypeptides polypeptides. The present sequence represents a human Nogo B phosphorothioate antisense oligonucleotide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  se; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renal cell carcinoma differentially expressed gene probe #4032.
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Claim 25; Page 32; 68pp; English
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non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear cells (FBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed). (MI) is useful for identifying genes that are differentially expressed in peripheral blood samples isolated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 88; antieense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; noctropic; neuroprotective; antiparkinsonian; muscular; D20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; g-cleaver; amberzyme; zinzyme; lrymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; Muman immundeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cherebrocytoma; acident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkingon's disease; ataxia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                     91.7%; Score 22; DB 12; Length 25; 77.3%; Pred. No. 1.1; 0; Indels iive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 8 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK02693 standard; RNA; 17 BP
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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(BLAT/) BLATT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOGO Amberzyme #365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                          Local Similarity 77.3
nes 17; Conservative
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                                                                                                                                                                                                                                                                   of the invention.
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Synthetic.
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cegulates expression of a neurite growth inhibitor gene (NGOD). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving an RNA molecule possessing an NGH motif), a G-cleaver (cleaving RNA with a NGH motif), a G-cleaver (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, he CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic CC leukaemia, HIV (human immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytocytopaenia, and inflammatory arthropathy. The NOGO gene in the presence of a divalent cation that is preferably Mg²+. Furthermore, the comprise of a divalent having a condition associated with the level of the cell and treat a patient having a condition associated with the level of the NoGO enter or man of the NOGO enter or more or a man or the nogo or more or a man or the nogo or more or a man or more or a man or more or a man or more or a man or more or a man or more or more or more or more or more or more or more or more or more or more or more or more or more or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present
growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is an amberzyme molecule of the invention
                                                                                                             Claim 88; Page 139; 200pp; English.
                                          central nervous system injury.
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70.8%; Score 17; DB 4; Length 17; 82.4%; Pred. No. 2.7e+02; tive 3; Mismatches 0; Indels Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other; Local Similarity 82.4 nes 14; Conservative Query Match Matches

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Gaps ö

> 22 17 ACCAGTGCCTCAGATAG 1 6 ACCAGUGCCUCAGAUAG ð 셤

ABK01533 standard; RNA; 17 BP ABK01533; RESULT 4

12-MAR-2002 (first entry)

Human NOGO Inozyme #803.

Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inDzyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens Synthetic

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cregulates expression of a neurite growth inhibitor gene (NGOD). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a maberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a NGN triplet), a zinzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA cyf CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, laukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, laukaemia, and inflammatory arthropathy. The NOGO gene in the presence of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the contacted with a vell to reduce NOGO activity of the contacted with a cell to reduce NOGO activity of the contacted with a vell to reduce not on on more cell and treat a patient having a condition associated with the level of the rear and patient having a condition associated with the level of therander. The presence of a new formulation mucleic acid may be contacted with a cell to reduce not not or more the rear a patient having a condition associated with the level of the rear manner. therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and , and/or other neurodegenerative disease modulation of NOGO expression. The present Gaps ö 70.8%; Score 17; DB 4; Length 17; 82.4%; Pred. No. 2.7e+02; tive 3; Mismatches 0; Indels Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other; sequence is an inozyme of the invention Chowrira BM; Claim 88; Page 90; 200pp; English. central nervous system injury. 11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. 09-FEB-2001; 2001WO-US004273. states which respond to the RIBOZYME PHARM INC. 14; Conservative 3latt L, Mcswiggen J, CHOWRIRA B M. BLATT L. MCSWIGGEN J. Best Local Similarity WPI; 2001-607195/69 WO200159103-A2. 16-AUG-2001. Query Match RIBO-) (CHOM/) (BLAT/) (MCSM/) Matches

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RESULT 5

ABK01534 standard; RNA; 17 BP ABK01534/c ID ABK015

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central nervous system injury.
             Synthetic.
            Homo
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treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present
                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                              sequence is an inozyme of the invention
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Best Local Similarity 76.55
Marches 13; Conservative
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                                                                                                                            (first entry)
                                                                                                                                                                                                    Human NOGO Inozyme #804.
                                                                                                                            12-MAR-2002
                                                    ABK01534;
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Gaps

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28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. 09-FEB-2001; 2001WO-US004273 11-FEB-2000; 2000US-0181797P RIBOZYME PHARM INC. MCSWIGGEN J. CHOWRIRA B M. BLATT L. WO200159103-A2 16-AUG-2001 (BLAT/) (MCSW/) (RIBO-)

sapiens.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and Chowrira BM; Blatt L, Mcswiggen J, WPI; 2001-607195/69.

Claim 88; Page 90; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cregulates expression of a neurite growth inhibitor gene (NGOD). The cregulates expression of a neurite growth inhibitor gene (NGOD). The cregulates expression of a neurite growth inhibitor gene (NGOD). The consessing an NGH motif), a G-cleaver (cleaving RNA with a NGW with an NGW triplet), a zinzyme (cleaving RNA with an NGW triplet), a zinzyme (cleaving RNA with an NGW triplet), a zinzyme (cleaving RNA with an NGW triplet), a zinzyme (cleaving RNA with an NGW triplet), a zinzyme (cleaving RNA cc of CD20 in the presence of a divalent cation that is preferably MG² +. C Purthermore, it may be contacted with a condition associated with the level conformed to the call and treat a patient having a condition associated with the level conformed in particular, the CD20 targetting nucleic acid may be used to treat lymphoma (NHL), bulky low-grade or follicular noncertangles. In particular, B-cell lymphoma, low-grade or follicular noncertangles. In munnocytoma (IMC), small B-cell lymphocytic lymphocytic lymphocytic lymphocytic lymphocytic acid is used to cleave RNA of the NGOO gene in the craspetting nucleic acid may be contacted with a cell to reduce NGOO gene in the craspetting nucleic acid may be contacted with a cell to reduce NGOO gene in the cell and treat a patient having a condition associated with the level of concot not more cell and treat a patient having a condition associated with the level of concot the rapies. In particular, the NGOO-targetting nucleic acid may be used to the use of one or more

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Human; se; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; noctropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; g-cleaver; amberzyme; zinzyme; Jymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; MC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; central nervous system injury; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; chemocherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkingon's disease; ataxia; Huntington's disease;
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70.8%; Score 17; DB 4; Length 17; 76.5%; Pred. No. 2.7e+02; ive 4; Mismatches 0; Indels
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ABK02081 standard; RNA; 17 BP
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06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                    Human NOGO Zinzyme #403.
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cc regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving a nn RNA molecule possessing an NCH motif), a G-cleaving RNA with a NYN motif) prossessing an NCH motif), a G-cleaving RNA with a NYN motif) prossessing an NCH motif), a G-cleaving RNA with a NYM motif) at CD20-targeting nucleic acid is used to cleaving RNA of CD20 in the presence of a divalent cation that is preferably MG<sup>2</sup>/+.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more condition associated with the level of CD20. The treatment may further comprise the use of one or more condition a lumphoma, leukaemia, B-cell lymphoma, IOW-grade or follicular non-Hodgkin's lymphoma , leukaemia, B-cell lymphoma, IOW-grade or follicular non-Hodgkin's lymphoma (MCL), immunocficiency virus) associated NHL, lymphocytic cut argeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>/+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the coll and treat a patient having a condition associated with the level of the theres are central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemories a witch respond to the modilation of NOGO expersesion. The present conserved is a vinxume molecular of the neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is a zinzyme molecule of the invention
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Gaps ; 0 Score 17; DB 4; Length 17; Pred. No. 2.7e+02; 0; Indels Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other; 3; Mismatches 70.8%; 82.48; Local Similarity 82.4 nes 14; Conservative Query Match Matches

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ABK01774 standard; RNA; 17 BP 12-MAR-2002 (first entry) ABK01774; ABK01774/c RESULT 7

Human NOGO Zinzyme #96.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; Jymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; Azkineon's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

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Homo sapiens. Synthetic.

WO200159103-A2

16-AUG-2001.

09-PEB-2001; 2001WO-US004273.

Renal cell carcinoma differentially expressed gene probe #4031.

ВР

RESULT 8

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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cegulates expression of a neurite growth inhibitor gene (NGOD). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid (e.g. a ribozyme or a makersyme (cleaving RNA with an NGW triplet), a zinzyme (cleaving RNA cyth a CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, if may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more cof CD20. The treatment may further comprise the use of one or more treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic Leukaemia, HTV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic, lumphoma, immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic, lumphoma, immunodeficiency virus) associated NHL, lymphoma, immunoteficiency arthropathy. The NOGO gene in the comprise of a divalent cation that is preferably Mg²+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce NOGO activity of the contacted with a cell to reduce now or more tharasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the use of none or more reduced to the parasise the u
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                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence is a zinzyme molecule of the invention
                                                                                                                                                                                                                                                             Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 88; Page 95; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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|||:|||:|||||||
17 CAGTGCCTCAGATAGGA 1
                                                                                                                    RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.8°
Best Local Similarity 82.4°
Matches 14, Conservative
                                                                                                                                                                                                                                                             Blatt L, Mcswiggen J,
                                                                                                                                                                       (MCSW/) MCSWIGGEN J. (CHOW/) CHOWRIRA B M.
                                                                                                                                            BLATT L.
MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                WPI; 2001-607195/69
                                                                                                                    RIBO-)
                                                                                                                                            (BLAT/)
  %XCCCCCCCCCCCCCCCCCCCCCCCCX
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peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                        Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                          Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
diagnosis; non-blood disease; solid tumor; gene expression;
                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4362; 350pp; English.
                                                                                               21-NOV-2003; 2003WO-US037481
                                                                                                                 21-NOV-2002; 2002US-0427982P.
03-APR-2003; 2003US-0459782P.
                                                                                                                                                                  ᄧᅜ
                                                                                                                                                       TWINE N C.
BURCZYNSKI M E
TREPICCHIO W L
                                                                                                                                                                                                                                                        WPI; 2004-460799/43.
                                                                                                                                                                                   (STOV/) STOVER J. SLON/) SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention
                                                        WO2004048933-A2
                                                                                                                                               AMHP ) WYETH
                                       Homo sapiens
                                                                            10-JUN-2004.
                                                                                                                                                                                                                          Twine NC,
Sloni DK;
                                                                                                                                                        (TWIN/)
(BURC/)
(TREP/)
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The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear calls (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed) (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene, that is differentially expressed and detected by the method ö Gaps ö 70.8%; Score 17; DB 12; Length 25; 82.4%; Pred. No. 2.9e+02; ive 3; Mismatches 0; Indels Sequence 25 BP; 4 A; 6 C; 4 G; 11 T; 0 U; 0 Other; 14; Conservative Local Similarity Query Match Matches

8 CAGUGCCUCAGAUAGGA 24

25 CAGTGCCTCAGATAGGA 9

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Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; ABKO1532/C
ID ABKO1532 standard; RNA; 17 BP.
XX
XX
XX
XX
XX
XX
XX
DF 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #802.
XX
XX
XX
KW Human; 88; antisense therapy; cy

cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; lorozyme;
Homo sapiens. Synthetic. WO200159103-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004273.

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

(RIBO-) RIBOZYME PHARM INC.

BLATT L. MCSWIGGEN J. CHOWRIRA B M. (BLAT/) (MCSW/) CHOW/)

Chowrira BM; Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 90; 200pp; English.

Expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGCO). The regulates expression of a neurite growth inhibitor gene (NGCO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids and nucleic acids and the a nucleic acids and the a nucleic acids and the an INN motif) and amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA cf coll to the real and treat a patient having a condition associated with the level coll to reduce CD20 activity of the cell and treat may further comprise the use of one or more cof CD20. The treatment may further comprise the use of one or more cof coll to particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (MMC), small B-cell lymphocytic lymphoma, immunocytoma (MMC), small acid is used to claave RNA of the NGCO gene in the cragetting nucleic acid may be condated with a cell to reduce NGCO activity of the collicie acid may be condated with a cell to reduce MCCO activity of the collicie acid may be condated with a cell to reduce NGCO activity of the collicie acid may be condated with a cell to reduce MCCO activity of the NGCO. The treatment may further comprise the use of one or more contral nervous system (CNS) injury and certoral acid acid sease, demental, muscular dystrophy, and/condated acid acid sease, centered or acid sease, ataxia, Huntingt sequence is an inozyme of the invention

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                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; notrie growth inhibitor gene; NOCO; hammerhead ribozyme; DNAzyme; inozyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Rodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaemia; stroke; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzhaimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease;
                                                                              Gaps
                                                                            ö
                                      Length 17;
                                  Score 16; DB 4; Length 17;
Pred. No. 8.2e+02;
3; Mismatches 0; Indels
Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chowrira BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system injury.
                                                                                                                                                                                                                                                      ABK02694 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                            Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2001; 2001WO-US004273.
                                                                                                                   24
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                                                                                                                                       17 AGTGCCTCAGATAGGA
                                                                                                                                                                                                                                                                                                                                 12-MAR-2002 (first entry)
                                                                                                                 9 AGUGCCUCAGAUAGGA
                                                                                                                                                                                                                                                                                                                                                                        Human NOGO Amberzyme #366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blatt L, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHOW/) CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-607195/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLATT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200159103-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                             ABK02694;
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the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more thereapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-foldskin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HV (human immunodeficiency virus) associated NHL, lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG'2+. Furthermore, the presence of a divalent cation that is preferably MG'2+. Furthermore, the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), Parkinson's disease, muscular dystrophy, and/or other neurodegenerative disease creates which respond to the modulation of NOGO expression. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a compound targeted to a nucleic acid molecule encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating diseases or conditions associated with aberrant expression or activity of Lck, such as hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lymphocyte specific tyrosine kinase (Lck) DNA PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 16; DB 4; Length 17; 75.0%; Pred. No. 8.2e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lymphocyte specific tyrosine kinase; Lck; PCR; ss;
antisense oligonucleotide; phosphorothicate linkage;
2.0-methoxyethyl sugar molety; 5-methylcytosine;
hyperproliferative disorder; cancer; cytostatic; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is an amberzyme molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; SEQ ID NO 6; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-2002; 2002US-00316515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-2002; 2002US-00316515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AUUCCACCAGUGCCUC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ATTCCACCAGTGCCTC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.v.
Then 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-498280/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP48303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP48303/
ID ADP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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surrounded by a jacket of permeable material with a porosity that allows release of the viral vector. The biocompatible capsules are implanted, e.g. into the central nervous system, for use in gene therapy, particularly where the active compound is useful in the treatment of

tumours, cancers and other cell proliferative diseases Sequence 30 BP; 6 A; 6 C; 7 G; 11 T; 0 U; 0 Other;

8888888

blood coagulation factor, or an enzyme. The biocompatible capsules are

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Gaps

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65.0%; Score 15.6; DB 2; Length 30; 59.1%; Pred. No. 1.4e+03; Live 5; Mismatches 4; Indels

13; Conservative

Local Similarity

Best Loc Matches

ઠ 셤

Query Match

:: ||| |:||||| |TTCACTTGTGGCTCAGATAGG 29 2 UUCCACCAGUGCCUCAGAUAGG 23

ABS68889 standard; DNA; 20

RESULT 13 **ABS68889**

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with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Lck polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents a PCR primer used to amplify DNA encoding a human Lck polypeptide of the
compound is an antisense oligonucleotide that specifically hybridises
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcl-2 gene; anti-apoptotic gene; prevention; cell death; treatment; neurodegenerative disease; disease; Huntingdon's; Parkinson's; Alzheimer's; retroviral vector; LNXS; LNCX; live packaging cell; biocompatible capsule; release; viral vector; implant; gene therapy; tumour; PCR primer; amplify; ss.
                                                                                                                                                                                                                          ö
                                                                                                                                                                                            Score 15.6; DB 12; Length 22;
Pred. No. 1.3e+03;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer 2 used in RT-PCR to amplify bc1-2 cDNA.
                                                                                                                                                                   Sequence 22 BP; 6 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      2 UUCCACCAGUGCCUCAGAUAGG 23
                                                                                                                                                                                                                                                                    22 TTACACCAATGCTTCAGATGGG 1
                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                65.0%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                    AAV05323 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-1998 (first entry)
                                                                                                                                                                                                             Local Similarity 59.1
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9744065-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                            invention.
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                                                                                                                                                                                                                             Matches
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Human; RecQ protein-like 4; RECQL4; ss; chromosome 8q24; infection; inflammation; tumour formation; cancer; cytostatic; antiinflammatory; antimicrobial; antisense therapy; antisense oligonucleotide.

Homo sapiens. US6436706-B1

20-AUG-2002.

23-FEB-2001; 2001US-00792594. 23-FEB-2001; 2001US-00792594.

(ISIS-) ISIS PHARM INC

Watt AT;

Ward DT,

97WO-US008463 96US-00650726

20-MAY-1997; 20-MAY-1996;

27-NOV-1997

(CYTO-) CYTOTHERAPEUTICS INC

Hammang JP, Aebischer P;

WPI; 1998-018231/02.

Human RecQ protein-like 4 (RECQL4) DNA antisense oligonucleotide #32

(first entry)

20-NOV-2002

ABS6889;

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New antisense compounds targeted to nucleic acids encoding RecQ protein-
like 4, useful for modulating expression of the nucleic acid and treating
diseases associated with expression of the nucleic acid in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a compound targeted to specific nucleobases of RecQ protein-like 4 (RECQL4) and which hybridises and inhibits the expression of RECQL4. The compound is useful for inhibiting the expression of RECQL4 in cells or tissues and for treating an animal, particularly a human suspected of having or being prone to a disease or condition associated with expression of RECQL4. The compound is useful for diagnostics, therapeutics and as a research reagent, e.g. prophylactically to prevent or delay infection, inflammation or tumour formation. This sequence represents an antisense oligonucleotide used in inhibition of human RECQL4 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Col 45; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-689941/74.
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vectors for gene

Capsule containing packaging cells that produce viral vectors for ger therapy - used as replaceable implants in treatment of cancer, atherosclerosis etc., providing localised, long-term vector delivery.

Example 5; Page 33; 45pp; English.

ö Gaps ö 64.2%; Score 15.4; DB 6; Length 20; 76.5%; Pred. No. 1.6e+03; ive 3; Mismatches 1; Indels 4 CCACCAGUGCCUCAGAU 20 Local Similarity 76.5 les 13; Conservative Query Match Best Loca Matches ò

PCR primers AAV05322-23 are used in a reverse transcription polymerase there reaction (RT-PCR) to amplify bcl-2 cDNA from human, rat, or mouse throws total RNA. Bcl-2 genes are anti-apoptotic genes whose products prevent unwanted death of certain cell populations, and are useful for treating neurodegenerative diseases such as Huntingdon's, Parkinson's or Alzheimer's disease. The PCR product was ligated into retroviral vectors LNXS and LNXX, to produce retroviral vectors LNXS-bcl-2 and LNXC-bcl-2. The vectors are used to transfect live packaging cells which form the secret a biocompatible capsule. These packaging cells which form the secret a viral vector which includes a heterologous gene (in this case bcl-2) encoding a biologically active compound e.g. antisense sequence,

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The present invention describes originalizated in describing messenger RNAs that populate a (sub-)transcripted from multiple transcription units that populate a genome. The library comprises several oligonuclectides, each capable of phyridising selectively to a set of messenger RNAs transcription unit of the genome, which encodes one or more messenger RNA splice variants. The encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a coligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or caracterising the corresponding transcriptor, and in certanscripts and splice variants of human or animal consecuting RNA transcripts and splice variants of human or animal consecuting RNA transcripts of a sub-transcriptome under a particular consecution or pathological state, and so allowing the detection of tissue to any pathology-specific genes such as those genes only expressed in specific genes; and to detect RNA transcriptome of a pathent suffering from a particular consecution. ABN27253 to ABNS9589 represent oligonuclectide sequences from cates, invention. N.B. The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format consecutive from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                       Human spliced transcript detection oligonucleotide SEQ ID NO:6841.
                                                                                                                                                                                                                                                           Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide libraries comprising oligonucleotides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 6841; 47pp; English.
1 CCACCAGTGCCTCAGGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2001; 2001WO-IB001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                                  ABN34093 standard; DNA; 60
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific genes.
                                                                                                                                                                                                                                                                                                                                                                WO200210449-A2
                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoshan A,
                                                                                                                                        ABN34093;
                                                        RESULT 14
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Score 15.4; DB 6; Length 60; Pred. No. 1.9e+03; 3; Mismatches 1; Indels Sequence 60 BP; 16 A; 10 C; 20 G; 14 T; 0 U; 0 Other; 64.2**%**; 76.5**%**; Query Match

22 6 ACCAGUGCCUCAGAUAG

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13; Conservative

Matches

Local Similarity

18 ||||||:|||:||| :||
ACCAGTGCCTCAGGTAG

Human SNP oligonucleotide #524. AAL27316 standard; DNA; 51 BP (first entry) 24-JAN-2002 AAL27316; RESULT 15 AAL27316

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; eucuporocetive; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thiossterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss

Homo sapiens.

WO200147944-A2.

05-JUL-2001,

28-DEC-2000; 2000WO-US035498.

28-DEC-1999; 99US-0173419P. 27-DEC-2000; 2000US-00173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

Claim 1; Page 1539; 4143pp; English

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptomets related proteins, cadherin, cyclin, polymerses, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune configurates (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic

Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;

Gapa ö 63.3%; Score 15.2; DB 4; Length 51; 70.0%; Pred. No. 2.3e+03; ive 3; Mismatches 3; Indels 14; Conservative Similarity Query Match Local Matches

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3 UCCACCAGUGCCUCAGAUAG 22 : || |||:|||:||| || 18 TCCGTCAGTGCCTCAGACAG 37

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Gaps

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Search completed: July 30, 2005, 15:45:04

Job time : 297.459 secs

AL940086 Arabidops AU103667 AU103667 AU10367 AU103667 AU30674 AU103674 AW36534 Bh27a03.y N29657 yw73c07.s1 CL528462 ASV13E10. AL545234 T. brucei AL555919 AL595919 AA705635 Zf40all.s AL44667 T. brucei AZ365377 IM0112E05 AZ365377 IM0112E05 AZ365377 IM0112E05 AZ3654151 SALK_0277

1M0030014 000818AAF

AV833686 AZ314162 CN849116 CN8493022 BZ767951 E

Pan trogl SALK 1395 Arabīdops AU103667

Tue Aug

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/mol_type="mRNA"
// Aref="taxon:9606"
// Abox="mRNA"
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E 1 (Dasses 1 to 31)

S 1 (Dasses 1 to 31)

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
Insert Length: 1006 Std Error: 0.00

Seg primer: -400P from Gibco

High quality sequence stops: 1.

Location/Qualifiers
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/organism="Homo sapiens"
                                                       AV833686
AZ314162
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AU102336 AU102336
                                                                                                                               July 30, 2005, 15:01:12 ; Search time 2331.57 Seconds (without alignments) 391.815 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        34239544 seqs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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BH851910
BC6032303
BC60328
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AZ6056211
AZ391620
AZ36596
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AZ365396
AZ165333
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24
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seq length: 60
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Mus musculus (bouse mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 50)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                              AZ452836 1000 50 bp DNA linear GSS 04-OCT-2000 1M0252H23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0252H23 R, genomic survey sequence.
304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                     Gaps
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                                                                                                                               Query Match 66.7%; Score 16; DB 1; Length 31; Best Local Similarity 66.7%; Pred. No. 9.2e+03; Matches 16; Conservative 3; Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunngemetics.utah.edu
Smatt.ength: 10000 Std Error: 0.00
Plate: 0252 row: H column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0252 row: H column: 23 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0252H23"
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shapered by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymuclecide kinase. Adaptor oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf rom a derivative
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Phose whole genome scaffolding with paired end reads from 10kb plasmid inserts
adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0252002R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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0
                                                                                                                                                                                 Length 50
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                                                                                                                                                                              Query Match 60.8%; Score 14.6; DB 8; Best Local Similarity 71.4%; Pred. No. 4.5e+04; Matches 15; Conservative 2; Mismatches 4;
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Pax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0252 row: O column: 02

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
fatrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0252002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           6 CCACCGGTGCCTCAGCCATGA 26
                                                                                                                                                                                                                                                                                                                                 4 CCACCAGUGCCUCAGAUAGGA 24
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Best Local Similarity
Matches 11; Conserva
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BF143628/c
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                       AZ595168 13-DEC-2000 1MA linear GSS 13-DEC-2000 1M0407C07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0407C07 R, genomic survey sequence.
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                 Gaps
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                                                                                                                 58.3%; Score 14; DB 8; Length 42; 63.6%; Pred. No. 8.4e+04; tive 3; Mismatches 5; Indels
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Insert Length: 1000 Std Error: C
Plate: 0407 row. C column: 07
Seq primer: CACACAGĞAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10090"
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21 TACCACCAGTCACTTAGACAGG 42
                                                                                                                                                                                                             2 UUCCACCAGUGCCUCAGAUAGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ595168.1 GI:11717358
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Unpublished (2000)
                                                                                                                                                                 14; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                         Local Similarity
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KEYWORDS
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AZ595168/c
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.B. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stops: 57.
High quality sequence stops: 57.
                                                                                                                                                                                                                                                                                                                                              BF143628 ST Dp mRNA linear EST 24-OCT-2000 601799985F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021725 5', mRNA sequence.
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/note="Organ: lung; Vector: pCWV-SPORT6; Site 1: Not1;
/note="Organ: lung; Vector: pCWV-SPORT6; Site 1: Not1;
Site 2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo MTV. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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58.3%; Score 14; DB 8; Length 44; 59.1%; Pred. No. 8.5e+04;
                                                                     4; Mismatches
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4021725"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from He Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
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with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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84112, USA
                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: C column: 07
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0397C07"
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Location/Qualifiers
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BH851910.1 GI:21422781
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                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 58) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HEMI Mouse EST Project
WashU-HEMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x CBA"
/db xref="taxon:10090"
/clone="IMAGE:552662"
                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
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xref="taxon:10090"
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BZ660828
BZ660828.1 GI:28173975
                                   sex="Male"
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                    Alonbo, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Geske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
L Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
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Bay Area Functional Genomics Consortium (BayGenomics)
Bayl: infoobaygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=RRX310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="SALK 073697.35.80.x"
/clone="SALK 073697.35.80.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 51)
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RRX310 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/ecotype="Col-0"
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Unpublished (2001)
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/strain="129 ola"
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BZ660828 11-JAN-2003 SALK 024289.23.50.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_024289.23.50.x, genomic
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/clone="SALK 024289.23.50.x"
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/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Decails of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
The Salk Institute for Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.

    (bases 1 to 56)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At1g04870.
                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
/note="Vector: pGT2Lxf"
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                          Length
                                                                                                                                                                   55.8%; Score 13.4; DB 9; 56.5%; Pred. No. 1.7e+05; tive 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                         Class: TDNA tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      2 UUCCACCAGUGCCUCAGAUAGGA 24
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0423 row: G column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 41.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UUGC1M0423G16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                         28 ACCAGTGCCGGTGATAGG 11
                                                                                                                                                                                                                                                                                                                                                          6 ACCAGUGCCUCAGAUAGG 23
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                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Best Local Similarity
Matches 13; Conserv
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Rocan, R., Materston, R., and Wilson, R., Jackson, Y., Cardenas, M.,
McCann, R., Materston, R., and Wilson, R.,
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Awe. Brockings, SD 57006 USA (phone: 800 423
4163; email: info@biogeneticservices.com)
How mailty each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /done lib="Gm-clodd"
//note="Vector: pBluescript II XR; Site_1: EcoRi; Site_2: Xhoi; Root canNa. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's CDNA Synthesis with (catalog #200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used (GAGAGAGAGAGAACAGACAGACAGAGAACTAGTCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The Xhoi site within the first-strand synthesis primer was restricted by digestion with Xhoi; all Xhoi sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs ware size-fractionated attue. The cDNA constructs were size-fractionated with a SOUDp cutoff, using GibcoRR Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and Xhoi, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possesse putative colonies 9n=15) have been sequenced, and possesse putative colonies ylaseria.
31 bp mRNA linear EST 23-JUL-2004 sa33h08.y1 Gm-c1004 Glycine max cDNA clone GENCOME SYSTEMS CLONE ID: Gm-c1004-1144 5' similar to TR:P93683 P93683 MEMBRANE INTRINSIC PROTEIN ;, mRNA sequence.
A1443458
A1443458.1 GI:4303310
EST.
                                                                                                                                                                                                                                                                                                                           Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-1144"
/lab_hoge="xtuo-gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                             Glycine max (soybean) Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine.
                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                  AI443458/c
LOCUS
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FEATURES

COMMENT

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil472114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 13-DEC-2000
Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 41).
I (bases 1 to 41).
Islam, A. Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ604085 13-DEC-200
1M0423G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clome_l1b="Mouse 10kb plasmid UUGCNM library"
/noce="Voctor: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                         55.0%; Score 13.2; DB 1; Length 31; 72.2%; Pred. No. 1.9e+05; ive 2; Mismatches 3; Indels
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Gaps

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55.0%; Score 13.2; DB 1; Length 61.1%; Pred. No. 2.1e+05; ive 4; Mismatches 3; Indels
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                                                                                                                                                                                                                3 UCCACCAGUGCCUCAGAU
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                                                                    Query Match
Best Local Similarity
Matches 11; Conserv
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Matches 12
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CC178725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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SOURCE
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-God (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GSP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligodar) primer of the primer and primer and of the primer and of the primer and of the primer and of the primer and of the primer and of the primer and of the primer and prim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 52)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pT713D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                    Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2110 Std Brror: 0.00
Seg primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                         Score 13.2; DB 8;
Pred. No. 2e+05;
4; Mismatches 3;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 bp
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/db_xref="taxon:9606"
/clone="1360121"
                                                                                                                                                                                                                                                                                                                                                                                      1 AUUCCACCAGUGCCUCAG 18
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                                                                                                                                                                                                                                         ch 55.0%;
l Similarity 61.1%;
11; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA782065
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AA782065/c
LOCUS
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                              Matches
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Oryzae;
Chases I to 52)
Brock, Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegu,B.,
Droc,G., Regad,F., Bourgeois,B., Meynard,D., Perin,C.,
Ghegquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
High throughput T-DNA insertion mutagenesis in rice: A first step
towards in sillco reverse genetics
Contact: Guiderdoni
UMR PIA Biotrop program
CL522553 12-APR-2004 SAM6B01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines Oryza sativa (japonica cultivar-group) genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fincte-PCR was performed on DNA of primary transformants of Orysa sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from june 2004 at http://genoplante-info.infobiogen.fr/oryzatagline/. This sequence has been generated in the framework of the Prench plant genomics program Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Flanking Sequence Tag of Oryza sativa T-DNA insertIon lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
| mol type="genomic DNA"
|cultivar="Nipponbare"
| db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE TEL: 3346/7615629
Fax: 3346/7615605
Email: emmanuel.guiderdoni@cirad.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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http://genoplante-info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.0%; Score 13.2; DB 9; 66.7%; Pred. No. 2.1e+05; iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: TDNA tagged.
Location/Qualifiers
                                                                                                                                       CL522553
CL522553.1 GI:46149353
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us-09-544-776-5.szlm60.rst

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Eukaryotta; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Experiments.

Experiments.

In (bases 1 to 53)

RS BayGenomics.

In (bases 1 to 53)

Experiments.

Ex
CC178725 53 bp mRNA linear GSS 02-MAY-2003
XA060 BayGenomics Gene Trap Library pGTOpfs Mus musculus CDNA, mRNA
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/organism="Mus musculus"
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/note="Vector: pGTOpfs"
                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
                                                                                                                                                         CCI78725
CC178725.1 GI:30317276
                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Search completed: July 30, 2005, 18:20:58 Job time : 2336.57 Becs

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Gaps

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ch 55.0%; Score 13.2; DB 8; Length 53; 1 Similarity 61.1%; Pred. No. 2.1e+05; 11; Conservative 4; Mismatches 3; Indel8

Best Local Similarity Matches 11; Conserva

Query Match

3 UCCACCAGUGCCUCAGAU 20

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6335, Ap 11, Appl 11, Appl 84552, A 94333, A

Sequence

ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

3484, Ap 8, Appli

US-09-705-267A-147 US-09-396-196G-50540 US-09-396-196G-62217 US-09-396-196G-70964 US-08-439-819-1 US-08-439-819-2 US-08-439-819-2 US-08-439-819-2 US-08-439-819-5 US-08-439-819-5 US-08-959-212-8 US-08-959-212-8 US-08-959-212-8 US-08-959-212-8 US-08-959-212-8 US-08-959-212-8 US-08-959-212-8 US-08-959-213-8 US-08-959-213-8 US-08-957-959-95 US-08-957-959-95 US-08-958-452A-6335 US-09-396-196G-84552 US-09-396-196G-94333

Appli Appli

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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Sequence 2, Appli
Sequence 1657, Appl
Sequence 102634,
Sequence 13, Appl
Sequence 12, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 81073, Appl
Sequence 81073, Appl
Sequence 81073, Appl
                                                                                                                                   (without alignments)
465.710 Million cell updates/sec
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                                                                                                                 July 30, 2005, 15:05:52 ; Search time 84.3243 Seconds
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-650-726-2
US-09-792-594-41
US-09-396-1966-10557
US-09-396-1966-10557
US-09-396-1966-105634
US-09-396-1966-105634
US-08-488-212A-43
US-08-408-011-43
US-08-306-1966-1073
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US-09-396-1966-10563
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US-09-396-1968-2-3
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US-09-71-975-267A-107
US-09-71-975-267A-107
US-09-986-621-30
US-09-986-621-30
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                                                                                                                                                                                                                                                                                                                                     1202784 segs, 818138359 residues
                                                                                                                                                                                                                                      1 auuccaccagugccucagauagga 24
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Maximum Match 100%
Listing first 45 summaries
                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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24
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Match Length
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0
                                                                                 APPLICANT: Hammang, Joseph P
APPLICANT: Hammang, Joseph P
APPLICANT: Aebischer, Patrick
TITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                                                                                                                   ZIP: 10020-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,726
FILING DATE: 20-MAY-1996
CLASSIFICATION: 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 15.6; DB 3; 59.1%; Pred. No. 2.8e+02; ive 5; Mismatches 4;
                                                                                                                                                                                                                ADDRESSEE: FISH & NEAVE
STREET: 1251 Ave. of the Americas
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: BIrifi, IVOR R
REGISTRATION NUMBER: 39,529
REFRENCE/DOCKET NUMBER: CII-3
TELEPHONE: 212 596 9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
US-08-650-726-2; Application US/08650726; Sequence 2. Application US/08650726; Patent No. 6027721; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.0
Best Local Similarity 59.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-650-726-2
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Sequence 37454, A Sequence 120549, Sequence 45, Appl Sequence 3, Appli

Sequence 107, App Sequence 3, Appli

Sequence 3, P Sequence 30, Sequence 3,

Sequence 30, Appl Sequence 30, Appl Sequence 119424,

Sequence 1 Sequence Sequence Sequence 6

37, Appl 64157, A

JS-09-396-196G-64157

US-08-169-715-53 US-08-737-607-37

13.88 13.88 13.88 13.88 13.66 13.66

Gaps

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Sequence 12, Application US/09249585A

Patent No. 6417002

GENERAL INFORMATION:
APPLICANT: HOLICK, Robert

TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905

CURRENT APPLICATION WHEER: 18/09/249,585A

CURRENT APPLICATION WHEER: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 32
                                                                                                                                                                                                                                                                                                                            63.3%; Score 15.2; DB 4; Length 25; 60.0%; Pred. No. 4.2e+02; Live 5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-396-83857/C

US-09-396-196G-83857/C

Sequence 83857, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.
TITLE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT PILING DATE: 1999-09-15

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE FABSES (for Windows Version 4.0

SEQ ID NO 83857

LENGTH: 25

LENGTH: 25

LENGTH: 25

LENGTH: 25
TITLE OF INVENTION: Methods of Genetic Analysis
                   FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 102634
LENGTH: 25
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1 ATTCAACCAGTGACTAAGAT 20
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ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.73
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                    US-09-396-196G-102634
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US-09-249-585A-12
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                                                                                                                                                                                      APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL4 EXPRESSION
FILE REFERENCE: 875-0209
CURRENT APPLICATION NUMBER: US/09/792,594
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 89
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.3%; Score 15.2; DB 4; Length 25; Best Local Similarity 70.0%; Pred. No. 4.2e+02; Matches 14; Conservative 3; Mismatches 3; Indels
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; Sequence 1657, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: Affwmetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; PILE REFERENCE: 31011.
; CURRENT FILING DATE: 1996-09-15
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEC ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Antisense Oligonucleotide US-09-792-594-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102644, Application US/09396196G
Patent No. 682174
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
  8 TTTCACTTGTGGCTCAGATAGG 29
                                                                                                                 // Bequence 41, Application US/09792594
// Patent No. 6436706
// GENERAL INFORMATION:
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22 ATGCCAGCAGTGCCACAGAT 3
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-1657
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                                                                       RESULT 2
US-09-792-594-41
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No. 5665355ember 8, 1991

PUBLICATION DATE:

; US-08-488-212A-43

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TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Other nucleotide useful in amplification of T Cell Receptor
MOLECULE TYPE: Va region)
HYPOTHETICAL: No
ORIGINAL SOURCE: Olygonucleotide synthesis machine
ORIGINAL SOURCE: oligonucleotide synthesis machine
PUBLICATION INFORMATION:
AUTHORS: Imberti, Luisa; Sottini,
AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
                                                                                                                                                                                                                                                                                     ö
i LOCATION: (1)..(32)
; OTHER INFORMATION: oligonucleotide used for RT-PCR amplification of Bcl2
US-09-249-585A-12
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TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
JOURNAL: Science
                                                                                                                                                                                          Length 32;
                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                Query Match 60.8%; Score 14.6; DB 3; Best Local Similarity 61.9%; Pred. No. 8.7e+02; Matches 13; Conservative 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS Onset
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 4/66

COMPUTER: 4/66

COMPUTER: Microsoft Word for Windows SOSTWARE: Microsoft Word for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,212A FILING DATE: 07-Jun-1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,485
FILING DATE: NO. 5665355mber 9, 1992
ATTONNEY/AGENT INFORMATION:
NAME: THOMAS E. POFOVICH
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3078
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compag Prolinea
COMPUTER: 4/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Thomas E. Popovich, Thomas ADDRESSEE: Popovich & Associates STREET: 80 South 8th Street CITY: Minneapolis STATE: Minnesota COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
18-08-488-212A-43
'Sequence 43, Application US/08488212A
'Patent No. 5665355
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12 TTCACTTGTGGCTCAGATAGG 32
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MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
MOLECULE TYPE: Va region)
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                                                                                                           0; Gaps
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TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
Query Match 59.2%; Score 14.2; DB 1; Length 24; Best Local Similarity 68.4%; Pred. No. 1.3e+03; Matches 13; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS ONSET
NUMBER OF SEQUENCES: 57
CORRESPONDENCES: 57
CORRESPONDENCES: FOODORICH, THOMAS
ADDRESSER: THOMAS E. POPOVICH, THOMAS
ADDRESSER: POPOVICH, & ASSOCIATES
STREET: 80 SOUTH 8th Street
CITY: Minneapolis
STATE: Minneapolis
STATE: Minneapolis
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ZIP: 55402-11

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: SLOXAGE
COMPUTER: 4/66
OPERATING SYSTEM: MS-DOS Version S
SOPERATING SYSTEM: MS-DOS Version S
SOPERATING SYSTEM: US/08/320,306
FILING DATE: 06-OCT-1994
CLASSIPICATION UMBER: 07/973 485
FILING DATE: No. 5891623ember 9, 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3678
TELEPHONE: (612) 334-8994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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Patent No. 5891623
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 5 ATTCAAACAGCGCCTCAGA 23
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TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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US-08-408-011-43
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Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selective Depletion in HIV Infection of T Cells That Bear Specific T Cell Receptor Vb Sequences
                                                                                                Gaps
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                                           59.2%; Score 14.2; DB 2; Length 24; 68.4%; Pred. No. 1.3e+03; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: No Synthesized using ORIGINAL SOURCE: Synthesized using ORIGINAL SOURCE: oligonucleotide synthesis machine PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                          RESULT 9
US-00-488-209B-43
; Sequence 43, Application US/08488209B
; Patent No. 5925313
; GENERAL INFORMATION:
; TITLE OF INVENTION: Daignosis and Treatment of TITLE OF INVENTION: Diagnosis and Treatment of Number OF SEQUENCES: S7
; CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: POPOVICh & Associates ADDRESSE: POPOVICh & Associates ADDRESSE: Popovich & Associates CITY: Minneapolis
; CITY: Minneapolis
; CITY: Minneapolis
; CITY: Minneapolis
; CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTRY: FILLEDOCAL
COMPUTRY READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea
COMPUTER: Storage
COMPUTER: 166
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488, 209B
FILING DATE: O'-UN-1995
CLASSIFICATION NUMBER: 07/973,485
FILING DATE: NO. 592513ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas B. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3678
TELECHOMONICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEPHONE: (612) 334-8994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
TYPE: Nucleic Acid
STANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSUE: 5033
PAGES: 860-862
PUBLICATION DATE: No. 5925513ember 8, 1991
                                                                                                                                             1 AUUCCACCAGUGCCUCAGA 19
                                                                                                                                                                       s ATTCAAACAGCGCCTCAGA 23
                                             Query Match 59.2
Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-488-209B-43
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AUTHORS:
AUTHORS:
JS-08-320-306-43
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Gest Local Staniarity 68 44; Pred. No. 1.34-01;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OV 1 AUTCHACAGGGCCTCAGA 2

RESULT 10

US-08-108-101-43

DESTINATION OF THE PRED. No. 1.34-01

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STREET: 00 SOUTH STANDAY OF THE PRED. NO. 1.34-01

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STREET: 00 SOUTH STANDAY OF THE PRED. NO. 1.34-01

STREET: 00 SOUTH STANDAY OF THE PRED. NO. 1.34-01

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                 Sequence 102633, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQTWARE: FRSEESEQ for Windows Version 4.0
SEQTWARE: 25
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US-09-396-196G-37454/C
; Sequence 37454, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; ATTLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37454
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 UCCACCAGUGCCUCAGAUAGGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ATTCAACCAGTGACTAAGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.2'
Matches 12; Conservative
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Best Local Similarity 63.6°
Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
  RESULT 13
US-09-396-196G-102633
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  Length 24;
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                                            3; Indels
                                                                                                                                                                                                        US-09-396-196G-81072/c

Sequence 81072, Application US/09396196G

Fatent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann:
APPLICANT: David Mack

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFRENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60100,678

PRIOR APPLICATION NUMBER: 60100,678

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOSTWARE: FRSESEQ for Windows Version 4.0
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; Sequence 81073, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: AFFMetrix, Inc.
; TITLE NEFERENCE: 3101.1
Query Match 59.2%; Score 14.2; DB 2; Best Local Similarity 68.4%; Pred. No. 1.3e+03; Matches 13; Conservative 3; Mismatches 3;
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Pred. No. 1.3e+03;
2; Mismatches 3;
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 81073
LENGTH: 25
                                                                                    1 AUUCCACCAGUGCCUCAGA 19
                                                                                                          5 ATTCAAACAGCGCCTCAGA 23
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73.7%;
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Best Local Similarity 73.74
Matches 14; Conservative
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Best Local Similarity 73.7
Matches 14; Conservative
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; ORGANISM: mus musculus
US-09-396-196G-81072
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US-09-396-196G-81073
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LENGTH: 25
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FILE REFERENCE: 3101.1
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-17
PRIOR PILING DATE: 1996-09-17
PRIOR PILING DATE: 1996-09-17
NUMBER OF SEQ ID NOS: 127806
SCFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120549
LENGTH: 25
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-120549
Query Match
Best Local Similarity 59.1%; Pred: No: 1.6e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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Search completed: July 30, 2005, 18:25:13 Job time : 85.3243 secs

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Sequence Sequence Sequence

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Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: mycla.
APPLICANT: myclael B.
APPLICANT: Twine, Natalie C.
APPLICANT: Twine, Natalie C.
APPLICANT: Twine, Natalie C.
APPLICANT: Dorner, Andrew J.
APPLICANT: Dorner, Andrew J.
APPLICANT: Slonim, Donna K.
APPLICANT: Slonim, Donna K.
TITLE OF INVENTY MATHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS FILE REFERENCE: AM101080L
CURRENT PEPLICANTION NUMBER: US 60/459, 782
PRIOR PELLING DATE: 2003-04-03
PRIOR PLILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 4904
SOFTWARE: Patentin version 3.2
LENGTH: 25
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                                               US-09-780-533A-2691

US-09-780-533A-2693

US-10-719-900-292913

US-09-780-533A-1532

US-10-719-900-48746

US-10-719-900-832455

US-10-719-900-832455

US-10-719-900-832455

US-10-719-900-832455

US-10-719-900-832455

US-10-719-900-832455

US-10-719-900-82659

US-10-719-900-82659

US-10-809-189-1657

US-10-809-189-1657

US-10-719-956-57018

US-09-780-533A-714

US-10-719-956-571795

US-10-719-956-571795

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Pred. No. 0.94;
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GENERAL INFORMATION:
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-717-597-4363
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Best Local Similarity
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US-10-717-597-4363/c
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Sequence 183480,
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183482,
183483,
183484,
                                                                                                                                                                                   July 30, 2005, 15:29:53; Search time 451.784 Seconds (without alignments) 343.829 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Cgn2_6/ptodata1/lpubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata1/lpubpna/USO9_PUBCOMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-956-157-183480
US-10-956-157-183481
US-10-956-157-183482
US-10-956-157-183483
US-10-956-157-183483
US-09-780-533A-1533
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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87.5
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1533, Ap

Sequence

Score

Result

122222

1264597

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Sequence Sequence Sequence Sequence

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Sequence 183483. Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Myeth

APPLICANT: Myeth

APPLICANT: Myeth

APPLICANT: Myeth

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

CURRENT PILING DATE: 2004-10-04

NUMBER: OS SO ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 183483

LENGTH: 25
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TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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                                                                                                                                                                                                                                                                5; Mismatches
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           FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 183482
LENGTH: 25
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Pred. No.
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Pred. No.
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Publication No. US20050118625A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 UUCCACCAGUGCCUCAGAUAG 22
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76.2%;
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Best Local Similarity 76.2%;
Matches 16; Conservative
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Best Local Similarity 76.2%;
Matches 16; Conservative
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Best Local Similarity 76.23
Matches 16; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-183483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ), ORGANISM: Probe Sequence
US-10-956-157-183484
                                                                                                                                                                   ; ORGANISM: Probe Sequence US-10-956-157-183482
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                                                                                                                                                     TYPE: DNA
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TITLE OF INVENTION: HUGLETC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 183481
                                                                                                                                                                                                                                           APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 183480
LENGTH: 25
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APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
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Pred. No. 2.9;
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   0; Indels
   5; Mismatches
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Pred. No.
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GENERAL INFORMATION: APPLICANT: Wyeth APPLICANT: Wyeth Milliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-956-157-183482/c
; Sequence 183482, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
                                                                                                                                                                     Sequence 183480, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
                                      1 AUUCCACCAGUGCCUCAGAUAG 22
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                                                                           22 ATTCCACCAGTGCCTCAGATAG
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1 Similarity 76.2%;
16; Conservative !
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Best Local Similarity 76.2%;
Matches 16; Conservative
   17; Conservative
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ORGANISM: Probe Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Probe Sequence
US-10-956-157-183480
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Best Local Similarity
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US-10-956-157-183480/c
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                                                                                                                                                                                                                               APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
   Matches
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Sequence 1774, Application US/09780533A Publication No. US20030060611A1 GENERAL INFORMATION:
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Best Local Similarity 82.4*
....hes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-780-533A-2081/c
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US-09-780-533A-1774/c
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                                                                                                                                                 Sequence 1533, Application US/09780533A

Sequence 1533, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Glowingen, Jim

APPLICANT: APPLICANT: Abarat

APPLICANT: Haeberli, Phed and Reagent for the Inhibition of NOGO Gene

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBHB00, 878-A (400/011)

CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT FILING DATE: 2000-102-09

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SEQ ID NOS: 6679

SEQ ID NO 1533

LENGTUANT 1133
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Publication No. US20030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MHERE, US/09/780, 533A
CURRENT PILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: US 60/181,797
FRIOR APPLICATION DATE: 2001-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.8%; Score 17; DB 10; Length 17; 76.5%; Pred. No. 2.5e+02;
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                   2 UUCCACCAGUGCCUCAGAUAG 22
                                         25 TTCCACCAGTGCCTCAGATAG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 UCCACCAGUGCCUCAGA 19
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1534
LENGTH: 17
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US-09-780-533A-1533
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Matches 13; Conserv
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US-09-780-533A-1533/c
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RESULT 9

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Sequence 2081, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Acwiggen, Jim
APPLICANT: Acwiggen, Jim
APPLICANT: Habberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REPRENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
SROITMARE: PatentIn version 3.0
SEQ ID NO 2081
JAPELICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwigen, Jim

APPLICANT: Chowrita, Bharat

APPLICANT: Haeberli, Pete

TITLE OF INVENTION' Method and Reagent for the Inhibition of NOGO Gene

TITLE OF INVENTION' MCMBER: US 400/011)

CURRENT APPLICATION NUMBER: US 60/181,797

PRIOR APPLICATION NUMBER: US 60/181,797

PRIOR PILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SOFTMARE: PatentIn version 3.0

SEQ ID NO 1774

LENGTH: 17
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Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.,

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim
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US-09-780-533A-2694/c
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APPLICANT: Twine, Natalie C.
APPLICANT: Twine, Natalie C.
APPLICANT: Trepicchio, William L.
APPLICANT: Trepicchio, William L.
APPLICANT: Trepicchio, William L.
APPLICANT: Slonim, Donna K.
APPLICANT: Stover, Jennifer A.
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
FILE REFERENCE: AMIOLOGOL
CURRENT FILING DATE: 2003-11-21
PRIOR PILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 4904
SOFTWARE: Patentin version 3.2
              APPLICANT: Haeberli, Peter TILLS OF INVENTION OF NOCO Gene FILE REFERENCE: MBHBOO, 378-4 (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PELING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SDFTWARES PATENTIN VERSION 3.0
LENGTH: 17
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US-10-719-900-292913/C
US-10-719-900-292913, Application US/10719900
; Sequence 292913, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4362, Application US/10717597; Publication No. US20040110221A1
; GENERAL INFORMATION:
APPLICANT: Wyeth
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Chowrira, Bharat
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; ORGANISM: Homo sapiens
US-10-717-597-4362
                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity
Matches 14; Conserva'
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US-10-717-597-4362/c
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LENGTH: 25
                                                                                                                                                                                                                                                                                     TYPE: RNA
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US-09-780-533A-1532/c

Sequence 1532, Application US/09780533A

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chownita, Bharat

APPLICANT: Acwingen, Jim

APPLICANT: Acwingen, Jim

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

PILE REFERENCE: MBHB00, 878-A (400/011)

CURRENT FILING DATE: 2000-02-01

PRIOR APPLICATION NUMBER: US 60/181, 797

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 6679

SEQ ID NOS: 6679

SEQ ID NOS: 6679

SEQ ID NO 1532

LENGTH. 17

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Publication NO. US20030660511A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Hackingen, Jim
APPLICANT: Hackingen, Jim
APPLICANT: Hackingen, Jim
APPLICANT: Hackingen, John
APPLICANT: Hackingen, John
APPLICANT: Hackingen, John
APPLICANT: Hackingen, John
APPLICANT: Hackingen, John
APPLICANT: Hackingen, John
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
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                                                                                                                                                                                                                                                 Length 25;
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PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 292913
LENGTH: 25
                                                                                                                                                                                                                                                                                                   Indels
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Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 15; Conservative 3; Mismatches 3;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2694
LENGTH: 17
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US-09-780-533A-1532
                                                                                                                                         TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-292913
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ORGANISM: Homo sapiens
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US-09-780-533A-2694
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ö 0; Gaps Query Match 66.7%; Score 16; DB 10; Length 17; Best Local Similarity 75.0%; Pred. No. 7.8e+02; Matches 12; Conservative 4; Mismatches 0; Indels

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Search completed: July 30, 2005, 18:48:38 Job time: 452.784 secs

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41315, A 21946, A 21946, A 21963, A 97462, A 97463, A 179966, 618759, 895386, 441174,

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567, App 1442, Ap 168271, 541175,

US-10-956-157-135597 US-10-653-827-239 US-10-653-827-239 US-10-795-002-46 US-10-956-157-21946 US-10-956-157-21946 US-10-956-157-21946 US-10-956-157-21946 US-10-956-157-97462 US-10-956-157-97463 US-10-956-157-97463 US-10-956-157-97463 US-10-956-157-97463 US-10-956-157-97463 US-10-719-956-269669 US-10-719-956-269669 US-10-719-956-21966 US-10-719-956-21175 US-10-719-956-21175 US-10-719-956-25447 US-10-719-960-876663 US-10-719-960-876663 US-10-719-900-976663 US-10-719-900-977663 US-10-751-736-25240 US-10-751-736-25240 US-10-751-736-25240 US-10-751-736-25240 US-10-751-754-30 US-10-751-754-30 US-10-751-754-30 US-10-751-754-30 US-10-719-900-630467 US-10-719-900-630467 US-10-719-906-630467 US-10-719-956-138250 US-10-719-956-347262

Sequence Sequence Sequence Sequence Sequence Sequence

6447, Ap 30, Appl 25240, A 25351, A 292748,

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21945, A 97461, A 38250, A 64979, A 347262,

Sequence

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630466, 613272

Sequence Sequence Sequence

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Sequence 329432, Application US/10719900
| Publication No. US20050026164A1
| GENERAL INPORMATION:
| APPLICANT: Value Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE PERERRORE: 3528.1
| CURRENT APPLICATION NUMBER: US/10/719,900
| CURRENT APPLICATION NUMBER: 60/427,808
| PRIOR PFILING DATE: 2002 11.20
| WUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.4%; Score 16.6; DB 21; Length 25; Best Local Similarity 60.9%; Pred. No. 6.4e+02; Matches 14; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-329432
US-10-719-900-329432
                                                             115.6
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Sequence 14572, A
Sequence 568, App
Sequence 21957, A
Sequence 21960, A
Sequence 97484, A
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                                                                                                                           (without alignments)
343.829 Million cell updates/sec
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                                                                                                            July 30, 2005, 15:29:53 ; Search time 470.608 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10P_PUBCOMB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-956-157-21957
US-10-956-157-21960
US-10-956-157-97484
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US-10-719-900-329433
US-09-908-975-14572
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      7287783 segs, 3236178273 residues
                                                                                                                                                                                                         caacuucaggauuccagauaugccc 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                        IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 60
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Sequence 21957, Application US/10956157
Sequence 21957, Application US/10956157
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 21957
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21960, Application US/10956157

Sequence 21960, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wheth

APPLICANT: Wheth

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

FILE REPERENCE: 031996-04300 (Am 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

LENGTH: 25
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     TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SCOTWARE: Patentin version 3.0
SEQ ID NO 568
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 16; DB 10; 75.0%; Pred. No. 1.2e+03;
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Best Local Similarity 75.vv
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Matches 15; Conservative
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US-10-956-157-21957
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                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-956-157-21960/c
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US-10-956-157-21957/c
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US-09-908-975-14572/C

US-09-908-975-14572/C

Sequence 14572 Application US/09908975

Publication No. US20030165843A1

GENERAL INFORMATION:
APPLICANT: WASSERWAN, Avi

APPLICANT: WASSERWAN, Alon
APPLICANT: MINTZ, Eli

APPLICANT: MINTZ, Liat

APPLICANT: MINTZ, Liat

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTOME

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTOME

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: UNMER: US 60/221, 507

PRIOR FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PATENT HOUSE: 32337

SOFTWARE: PATENT HOUSE: 20337

SEQ ID NO 14572

LENGTH: 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 25;
                                                                                           APPLICANT STATEMENT TO THE STATEMENT OF THE STATEMENT OF TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 35.28 PILES REFERENCE: 35.28 PILES REPELICATION NUMBER: US/10/719,900 CURRENT FILING DATE: 2003-11-20 PRIOR PILING DATE: 2002 11 20 NUMBER OF SEQ ID NOS: 982914 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 329433 LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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64.8%; Score 16.2; DB 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 12; Conservative 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.4%; Score 16.6; DB 21
Best Local Similarity 60.9%; Pred. No. 6.4e+02;
Matches 14; Conservative 5; Mismatches 4
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US-09-780-533A-568/c
Sequence 568, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
PAPLICANT: Ribozyme Pharmaceuticals, Inc.
US-10-719-900-329433
; Sequence 329433, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CATCTTCCGGATGCTAGATATGC 23
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23 TTCACGGTTCCAGATATTCCC 3
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Chowrira, Bharat
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-329433
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APPLICANT:
APPLICANT:
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Publication No. US20040152168A1
GENERAL INFORMATION:
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: NEUROGENIN3 AND PRODUCTION OF PANCREATIC
TITLE OF INVENTION: ISLET CELLS
FILLE REFERENCE: UCSF-129CIP2
CURRENT APPLICATION NUMBER: US/10/795,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 60;
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TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS FILE REFERENCE: D0211 NP CURRENT APPLICATION NUMBER: US/10/453,827 CURRENT PILING DATE: 2003-06-03 CURRENT PILING DATE: 2003-06-03 PRIOR FILING DATE: 2002-06-03 NUMBER OF SEQ ID NOS: 1219 SOFTWARE: Patentin version 3.2 SEQ ID NO 239 LENGTH: 41
                                                                                                                                                                                                                                                    Score 16; DB 18; Le
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.0%; Score 16; DB 19; Best Local Similarity 58.3%; Pred. No. 1.3e+03; Matches 14; Conservative 5; Mismatches 5
                                                                                                                                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                 US-10-453-827-239
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                                                                                                                                                                                      TITLE OF INVENTION: William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOMETHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 97484
LENGHH: 25
TYPP: ...
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       Length 25;
   Query Match. 64.0%; Score 16; DB 21; Length 25
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels
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; PUDLication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
                                                                               1 CAACUUCAGGAUUCCAGAUAUGCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAACUUCAGGAUUCCAGAUAUGCC 24
                                                                                                   25 CCACTCCAGGATGTCAGATATGAC 2
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Best Local Similarity 75.0
Matches 12; Conservative
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US-10-956-157-135597
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US-10-956-157-135597/c
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US-10-956-157-97484/c
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US-10-453-827-239/c
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Sequence 21947, Application US/10956157

Sequence 21947, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: WUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER: PEACHLING DATE: 2004-10-04

NUMBER: PEACHLING PATE: 2014-10-04

SOFTWARE: PATENTING VERSION 3.2

SEQ ID NO 21947

LENGTH: 25
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Sequence 21963, Application US/10956157
Sequence 21963, Application US/20050118625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 21963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.4%; Score 15.6; DB 21; Length 25; 63.6%; Pred. No. 1.9e+03;
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                                                                                                                                                   Query Match 62.4%; Score 15.6; DB 21;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
Matches 14; Conservative 4; Mismatches 4;
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                                                                                                                                                                                                                                                         1 CAACUUCAGGAUUCCAGAUAUG 22
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Best Local Similarity 63.67
Matches 14; Conservative
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US-10-956-157-21963
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; ORGANISM: Probe Sequence
US-10-956-157-21947
                                                     TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-21946
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  SEQ ID NO 21946
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APPLICANT: Wounts, William

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION VNDHER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805
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; Sequence 41315, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REPERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR PELING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Miscroarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41315
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.0%; Score 16; DB 19; Length 60; Best Local Similarity 58.3%; Pred. No. 1.3e+03; Matches 14; Conservative 5; Mismatches 5; Indels
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US/10/642,093
PRIOR PILIG DATE: 2003-08-14
PRIOR FILING DATE: 2003-08-14
PRIOR PILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: PCT/USO2/11166
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 46
LENGTH: 60
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Publication No. US20050118625A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 59.1
Matches 13, Conservative
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; ORGANISM: Mus musculus
US-10-719-900-41315
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Search completed: July 30, 2005, 18:48:37 Job time: 471.608 secs

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Sequence Sequence Sequence

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Query Match
Best Local Similarity
Matches 18; Conserv
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US-10-956-157-169389
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ORGANISM: Probe
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                                                                                                    July 30, 2005, 15:29:53; Search time 470.608 Seconds (without alignments) 343.829 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-719-900-63085
US-10-956-157-164478
US-10-956-157-164480
US-10-956-157-164481
US-10-956-157-164481
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 7287783 seqs, 3236178273 residues
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                                                                             nucleic search, using sw model
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Maximum Match 10
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Maximum DB seq length: 60
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Perfect score:
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ALIGNMENTS

Sequence 851430,

Sequence Sequence Sequence

US-10-719-956-412824 US-10-719-900-73849 US-10-719-900-851430

US-10-719-900-619461

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APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERBNCE: 031895-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARES PATENTIN VERSION 3.2
SEQ ID NO 169389
LENGTH: 25
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7; Mismatches
Sequence 169389, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
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llarity 72.0%;
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Sequence 63085, A Sequence 164478, Sequence 164480, Sequence 164480, Sequence 164481,

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Sequence 164481, Application US/10956157

Sequence 164481, Application US/10956157

Sequence 16481, Application No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT RILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PatentIN version 3.2

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 164480
LENGTH: 25
                                                                                              DB 21; Length 25;
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                                                                                              96.0%; Score 24; DB 70.8%; Pred. No. 0.1; ive 7; Mismatches
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70.8%;
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Best Local Similarity 70.8%;
Matches 17; Conservative
                                                                                                                    Best Local Similarity 70.8
Matches 17; Conservative
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Best Local Similarity 70.8
Matches 17; Conservative
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US-10-956-157-164480
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ORGANISM: Probe Sequence
                      ; ORGANISM: Probe Sequence
US-10-956-157-164479
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US-10-956-157-164482/c
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US-10-956-157-164480/c
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; TYPE: DNA
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US-10-956-157-164479/c

Sequence 164479, Application US/10956157

Sequence 164479, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

APPLICANT: Wounts, WILLIAM

TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION WHORE: US/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 164479
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Publication No. US20050118625A1
GENERAL INFORMATION:
BEDELICANT: World:
APPLICANT: Wounte, William
TITLE OF INVENTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES
TITLE OF INSTRUCTION: HUMAN OSTEOARTHRITS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
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            Sequence 63085, Application US/10719900
; Publication No. US200050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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Pred. No. 0.1;
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SOFWARE: Patentin version 3.2
SEQ ID NO 164478
LENGTH: 25
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70.8%;
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; ORGANISM: Probe Sequence
US-10-956-157-164478
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus US-10-719-900-63085
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Best Local Similarity
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  US-10-719-900-63085/c
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APPLICANT: Wyeth

APPLICANT: Wyeth

APPLICANT: Wounts, William

APPLICANT: MOUNTS, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031865-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-110-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 158471
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Pred. No. 2.16+02;
5; Mismatches 3; Indels (
                                                                   DB 22; Length 25;
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 169643
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                                                               Query Match 79.2%; Score 19.8; D
Best Local Similarity 65.2%; Pred. No. 12;
Matches 15; Conservative 6; Mismatches
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Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 158471, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:
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Best Local Similarity 63.6%;
Matches 14; Conservative
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US-10-719-956-169643
  ; ORGANISM: Rattus norvegicus
US-10-719-956-169644
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Best Local Similarity
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US-09-780-533A-561/c
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                                                            APPLICANT: Wyeth Mounts, William APPLICANT: Wyeth Mounts, William APPLICANT: Wyeth Mounts, William APPLICANT: Wounts, William ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION NUMBER: US/10/956,157 CURRENT PILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 NUMBER OF SEQ ID NOS: 319805
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 169644, Application US/10719956
; Sequence 169644, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OP INVENTION: Methods of Genetic Analysis of Rat
; TILE REPERENCE: 3527.1
; CURRENT PAPLICATION NUMBER: US/10/719,956
; CURRENT PILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 25;
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Pred. No. 0.63
7; Mismatches
Sequence 164482, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
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70.8%;
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Best Local Similarity 66.7%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.89
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-164482
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US-10-719-900-63086
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                                                                                                                                                                                                                                                                     SEQ ID NO 164482
LENGTH: 25
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Sequence 1429, Application US/09780533A

Publication No. US20030606611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Achira, Bharat

APPLICANT: Haeberli, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBHBOO, 878-A (400/011)

CURRENT PILING DATE: 2001-02-03

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1429
                                     APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowrita, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MRHB00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 561
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Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrigan, Jim
APPLICANT: Chowriga, Sharat
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17 ATAGCTTGGATCACACC 1
Publication No. US20030060611A1
GENERAL INFORMATION:
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McSwiggen, Jim
Chowrira, Bharat
Haeberli, Pete
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Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-780-533A-561
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US-09-780-533A-1429/c
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US-09-780-533A-1430/c
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| Sequence 1737, Application US/09780533A
| Publication No. US20030060611A1
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Blatt, Larry
| APPLICANT: Chowrira, Bharat
| APPLICANT: Chowrira, Bharat
| APPLICANT: Habberll, Pete
| TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
| TITLE OF INVENTION: Method and Reagent for CURRENT APPLICATION NUMBER: US/09/780, 533A
| CURRENT PLILING DATE: 2001-02-09
| PRIOR APPLICATION NUMBER: US 60/181,797
| PRIOR FILING DATE: 2000-02-11
| NUMBER OF SEQ ID NOS: 6679
| SEQ ID NOS: 6679
| SEQ ID NOS: 6679
| SEQ ID NO 1737
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
LENGTH: 17
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Pred. No. 2.5e+02;
5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGAUAGCUUGGAUCACA 19
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70.6%;
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Matches 13; Conservative
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Best Local Similarity 70.6
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-780-533A-1737
                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Homo sapiens
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Sequence 31372, Sequence 31372

Sequence 1, Appli Sequence 5, Appli Sequence 62, Appli Sequence 62, Appli Sequence 1705, Ap Sequence 5, Appli Sequence 31, Appli Sequence 310, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 60, Appl Sequence 132, Appl Sequence 136, Appl Sequence 1960, Appl Sequence 156, Appl Sequence 156, Appl Sequence 156, Appl Sequence 9762, Appl Sequence 9763, Appl Sequence 10, Appl

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Sequence:

Minimum DB Maximum DB

Database

Searched:

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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2005
3 US-10-085-783A-54131

3 US-10-085-783A-31372

1 US-10-242-535A-31372

1 US-10-437-931-1

1 US-10-37-669-5

1 US-10-347-669-5

1 US-10-347-669-5

1 US-10-347-669-5

1 US-10-956-157-1705

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1 US-10-956-157-1305

1 US-10-972-593A-5

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1 US-10-974-846-132

1 US-10-974-846-132

1 US-10-974-846-132

1 US-10-974-846-132

1 US-10-976-157-9765

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1 US-10-956-157-976

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CURRENT FILING DATE: 2002-09-12
PRIOR PRILING DATE: 2002-09-12
PRIOR FILING DATE: 2001-02-28
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PLING DATE: 2001-03-12
PRIOR PLING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-14
SOFTWARE: PATCHING DATE: 2010-03-14
NUMBER OF SEQ ID NOS: 56994
SOFTWARE: PATCHING VERSION 3.2
LENGTH: 144
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Best Local Similarity 79.2%; Pred. No. 0.11
Matches 19; Conservative 5; Mismatches
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APPLICANT: ChondroGene Inc.
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US-10-242-535A-33274/c
      US-10-242-535A-33274
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ORGANISM: Human
         4444444444444444444444444444444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/NS07 PUBCOMB.seq:*

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8: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

17: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

18: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

19: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US10P PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-242-535A-57815
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US-10-085-783A-28762
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Maximum Match 100%
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Sequence 2876.2, Application US/10242535A

Sequence 2876.2, Application No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: Chordrodene Inc.

APPLICANT: Chordrodene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT PILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 28762

SEQ ID NO 28762
                                                                                                              Sequence 57815, Application US/10085783A
; Sequence 57815, Application No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Chondrodene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
; CURRENT PAPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-03-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; RIOR FILING DATE: 2001-03-12
; ROUTWARE: PatentIn version 3.2
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Best Local Similarity 79.2%; Matches 19; Conservative 5;
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Matches 19; Conservative
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ORGANISM: Human
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Sequence 57815, Application US/10242535A

Publication No. US20040003663A1

GENERAL INFORMATION:

APPLICANT: Chondrodene Inc.

APPLICANT: Chondrodene Inc.

APPLICANT: Chondrodene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT PILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,783

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFFWARE: PatentIn version 3.2

LENGTH: 170
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| GENERAL INFORMATION:
| APPLICANT: ChondroGene Inc.
| APPLICANT: ChondroGene Inc.
| APPLICANT: Liew, C.C.
| TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
| TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
| FILE REFERENCE: 4231/2002.
| CURRENT APPLICATION NUMBER: US 60/305,340
| PRIOR APPLICATION NUMBER: US 60/275,017
| PRIOR FILING DATE: 2001-03-12
| PRIOR FILING DATE: 2001-02-28
| NUMBER OF SEQ ID NOS: 58994
| SOFTWARE: PATCHTION VANBER: US 60/271,955
| SEQ ID NO 33274
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100.0%; Score 24; DB 17; Length 170;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels
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; Sequence 33274, Application US/10085783A
; Publication No. US20040037841A1
                                                           1 AUUCCACCAGUGCCUCAGAUAGGA 24
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US-10-242-535A-57815/c
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; ORGANISM: Human
US-10-085-783A-33274
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ORGANISM: Human
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Publication No. US20040037841A1
                                   GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
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                                   sequence 28762, Application US/10085783A

sequence 28762, Application No. US20040037841A1

general information:
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
APPLICANT: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
FRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
SPRIOR FILING DATE: 2001-03-14
SOFTWARE: PALENT ON NUMBER: US 60/271,955
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PALENT VERSION 3.2
LENGTH: 191
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Sequence 5.4131, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT PELLOATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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Pred. No. 0.11;
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Pred, No. 0.11;
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US-10-085-783A-54131/c
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US-10-242-535A-54131
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ORGANISM: Human
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT PILING DATE: 2002-02-28
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ### AFFLICANT: Lidew, C.C.

#### TITLE OF INVENTION: Compositions and Methods Relatiing to Osteosrthritis

#### FILE REFERENCE: 4231/2005

#### CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

#### PRIOR APPLICATION NUMBER: US 60/305,340

#### PRIOR FILING DATE: 2001-07-13

### PRIOR FILING DATE: 2001-07-13

### PRIOR FILING DATE: 2001-07-13

### PRIOR APPLICATION NUMBER: US 60/275,017

### PRIOR APPLICATION NUMBER: US 60/271,955

### PRIOR FILING DATE: 2001-02-28

### NUMBER OF SEQ ID NOS: 58994

### SOFTWARE: PatentIn version 3.2

### SEQ ID NO 31372
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5; Mismatches
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US-10-242-535A-31372/c
Sequence 31372, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: Chondrogene Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 ATTCCACCAGTGCCTCAGATAGGA 290
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100.0%;
Best Local Similarity 79.2%;
Matches 19; Conservative 5;
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Best Local Similarity 79.2%;
Matches 19; Conservative 5
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Gaps

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0; Indels

5; Mismatches

Score 24; DB 9; Length 1610; Pred. No. 0.12;

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Query Match
Best Local Similarity 79.2%; |
Matches 19; Conservative 5.
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ORGANISM: human
                                               TYPE: DNA
CRGANISM: human
US-09-765-205-5
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                              LENGTH: 1610
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          SEQ ID NO 5
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REPERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT PILING DATE: 2002-28
PRIOR FILING DATE: 2001-02-28
PRIOR PELICATION NUMBER: US 60/305,340
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
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Sequence 5, Application US/09765205
Patent No. US20020034800A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458-004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PastSEQ for Windows Version 3.0
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US-10-437-21-1/c
| US-10-437-21-1/c
| Sequence 1, Application US/10437931
| Publication No. US20030215868A1
| GENERAL INFORMATION:
| APPLICANT: Seeman, Philip
| APPLICANT: Tallerico, Teresa
| TILLE OF INVENTION: Wethod of Detecting Schizophrenia
| FILE REFERENCE: 13459-1
| CURRENT PAPLICATION NUMBER: US/10/437,931
| CURRENT FILING DATE: 2003-05-15
| PRIOR PILING DATE: 2003-05-16
| NUMBER OF SEC ID NOS: 6
| SOFTWARE: Patentin Version 3.1
| SEC ID NO: 1
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Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches
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Best Local Similarity 79.2*
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-10-437-931-1
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ORGANISM: Human
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US-09-765-205-5/c
                                                                                                                                                                                                                                                                                     SEQ ID NO 31372
LENGTH: 468
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TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLECTIDES
FILE REPERENCE: 1459.004/200130.449
CURRENT APPLICATION NUMBER: US/10/347,669
CURRENT FILING DATE: 2003-01-16
PRIOR PPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASELSEQ for Windows Version 3.0
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; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; General INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Mancy J
; TITLE OF INVENTION: Wethod for Predicting Autoimmune Disease
; FURREY APPLICATION WUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION WUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 62:
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Pred. No. 0.12;
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1 AUUCCACCAGUGCCUCAGAUAGGA 24
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Best Local Similarity 79.2%; F
Matches 19; Conservative 5;
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Matches 19; Conserv
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RESULT 15

US-10-956-157-1705/c

US-10-956-157-1705/c

Sequence 1705, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Woute, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 1705

LENGTH: 1785

LENGTH: 1785

TYPE: DNA

ORGANISM: Homo sapiens
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Search completed: July 30, 2005, 15:29:44 Job time : 463.784 secs

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TYPE: DNA
ORGANISM: Zea mays
RESULT 1
US-09-294-093B-149/c
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Sequence 149, App
Sequence 117468,
Sequence 280, App
Sequence 173, App
Sequence 8669, Ap
Sequence 11019, A
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| cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO7 NEW PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-99-722-280

US-09-960-352-8669

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US-09-960-352-8672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Applications NA:*
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Maximum Match 100%
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score greater than or equal to
and is derived by analysis of
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Maximum DB seq length: 2000000000
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402
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APPLICANT: Lalgudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

APPLICANT: Ito, Laura, Y.

APPLICANT: Ito, Laura, Y.

TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

CURRENT APPLICATION NUMBER: US/09/294,093B

CURRENT FILING DATE: 1999-04-16

FRIOR APPLICATION NUMBER: 60/082,567

FRIOR PILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 149

LENGTH: 270

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; OTHER INFORMATION: Incyte ID No. US20010051335A1 700342237H1
US-09-294-093B-149
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US-10-893-315-135

US-10-893-315-159

US-10-893-315-159

US-10-893-315-159

US-10-893-315-164

US-10-741-600-1761

US-10-741-600-1761

US-10-741-600-1761

US-10-741-600-1761

US-10-721-632-90568

US-10-027-632-90568

US-10-027-632-90568

US-10-027-632-90568

US-10-027-632-90568

US-10-1288-138-13

US-10-388-138-13

US-10-388-138-13

US-10-388-138-13

US-10-388-138-13

US-10-388-138-13

US-10-956-157-904

US-10-957-13823
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US-10-972-079-58889
US-09-851-682A-2
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Best Local Similarity 62.5%; Pred. No. 46;
Matches 15; Conservative 6; Mismatches 3;
  1830121
1830121
1830121
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US-10-775-169-173/c
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US-09-960-352-8669
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                                                                               RESULT 2
US-10-425-115-117468/c
US-10-425-115-117468, Application US/10425115
Fublication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 39-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 117468
LENGTH: 597
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APPLICANT: Morris, David
APPLICANT: Expelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30;
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR PELLING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.1
SEQ ID NO 280
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US-10-425-115-117468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.8%; Score 19.2; D
Best Local Similarity 62.5%; Pred. No. 49;
Matches 15; Conservative 6; Mismatches
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46 ATCTTCAGCATTCCAGATATGACC 23
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
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RESULT 4

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Sequence 11019, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nangbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE AND PAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
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Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAI DEPOSITION
FILLE OF INVENTION: MUSCLE AND FAI DEPOSITION
FILLE OF INVENTION: 10511.006/37-21 (10299)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
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APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, william
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REPERBYCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT APPLICATION DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 86574
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; GGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 37-LIB34-021-Q1-E1-B2
US-09-960-352-8669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.6; DB 9;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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Sequence 173, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 16; Conservative
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t,
                                                      TYPE: DNA ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,
                                                                                                                         NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals
    SEQ ID NO 1
LENGTH: 1830121
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GENERAL INFORMATION:

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION THEREOF.

TITLE OF INVENTION THEREOF.

TITLE OF INVENTION THEREOF.

TITLE OF INVENTION UNMER: US/10/329,670

CURRENT APPLICATION NUMBER: US/09/643,990

PRIOR PILING DATE: 2000-08-23

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5872. Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Weeley C.

APPLICANT: Warren, Weeley C.

APPLICANT: Machialagan, Nagappan

APPLICANT: Machialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT APLICATION NUMBER: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                DB 9; Length 402;
                                                                                                                                                                                                                                                                                            4; Indels
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NAME/KEY: unsure

LOCATION: (346)...(347)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: 25-LIB34-036-Q1-E1-G1
US-09-960-352-5872
                                                                                                                      TYPE: DNA CRGANISM: Bos taurus CTHER INFORMATION: Clone ID: 47-LIB34-022-Q1-E1-D4 US-09-960-352-11019
                                                                                                                                                                                                                                             Query Match 74.4%; Score 18.6; D
Best Local Similarity 64.0%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11019
LENGTH: 402
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a, t, g or c υ FEATURE: NAME/KEX; misc_feature LOCATION: (102596)..(102696) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc_feature LOCATION: (117136)..(117136) DTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (122167)..(122167) OTHER INFORMATION: n equals a, t, g or LOCATION: (51805)..(51805) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (131360)..(131360) OTHER INFORMATION: n equals a, t, g თ b NAME/KEY: misc feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals a, t, FEATURE: NAME/KEY: misc_feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a, t, FEATURE: NAME/KEY: misc_feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (653]3)..(65313) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (122336)...(122336) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (55369)..(55369) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (51805)..(51 NAME/KEY: misc_feature

ö Gaps Length 1830121; ö Indels Score 18.6; DB 17; Pred. No. 2.1e+02; 5; Mismatches 1071778 CAACTICAGGAIGCCCTITAIGCCC 1071754 FEATURE:
NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a, t, g or c OTHER INFORMATION: n equals a, t, g or c t, gor c 1 CAACUUCAGGAUUCCAGAUAUGCCC 25 b t, g NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (147197)..(147197) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (140398)...(140398) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (145058)..(145058) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a, Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative NAME/KEY: misc feature LOCATION: (145942)..(145942) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (152530)..(152530) LOCATION: (139910) .. (139910) 셤 ò

Sequence 1, Application US/10158865

Sequence 1, Application No. US2004020393A1

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragr
TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: WIMBER: US/10/158,865

CURRENT APPLICATION NUMBER: US 09/557,884

PRIOR PILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTHAL 1830121

LENGTHAL 1830121 RESULT 9 US-10-158-865-1/c

ORGANISM: Haemophilus influenzae PERJURE: NAME/KEY: misc feature LOCATION: (4747)..(4747)

TYPE: DNA

FEATURE:
NAME/KER:
MANG/KER: misc_feature
COTATION: (55369)..(55369)
OTHER INFORMATION: n equals a,t,c, or g NAME/KEY: misc feature LOCATION: (36543)..(36543) OTHER INFORMATION: n equals a,t,c, or g WAME/KEY: misc feature COCATION: (36636)..(36636) OTHER INFORMATION: n equals a,t,c, or g NAME/KEY: misc feature LOCATION: (40808)..(40810) JTHER INFORMATION: n equals a,t,c, or g FEATURE: NAME/KEY: misc_feature LOCATION: (36551). (36551) OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (29298)..(29298) OTHER INFORMATION: n equals a,t,c, or MANE/KEX: misc feature OCATION: (44975)..(44975) WHER INFORMATION: n equals a,t,c, or ö ö NAME/KEY: misc_feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals a,t,c, or FEATURE: or or ö NAME/KEY: misc feature
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a,t,c, or
FRATURE:
NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,t,c, or FEATURE: misc_feature NAME/KEY: misc_feature COCATION: (44416) ...(44416) OTHER INFORMATION: n equals a,t,c, IAME/KEY: misc_feature CCATION: (44905)..(44905) YTHER INFORMATION: n equals a,t,c, FATURE: FEATURE: NAME/KEY: misc feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (47036)..(47036) THER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (51602)..(51602) OTHER INFORMATION: n equals a,t,c, FEATURE:
NAME/KEY: misc_feature
LCCATION: (51786)..(51786)
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NAME/KEY: misc feature LOCATION: (140398)..(140398) OTHER INFORMATION: n equals a,t,c, or g FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals a,t,c, or FRATURE: NAME/KEY: misc feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a,t,c, or FRATURE:
NOGATION: (102596)...(102696)
OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (117136)..(117136) OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a,t,c, or ö FEATURE:
MANG/KEY: misc_feature
LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (120038)...(120038) OTHER INFORMATION: n equals a,t,c, FEATURE:
NAME/KEY: misc_feature
LCCATION: (113910). (113910)
OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (122167)...(122167) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc_feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (65313)..(65313) OTHER INFORMATION: n equals a,t,c, FEATURE: FEATURE:

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NAME/KEY: misc feature
LOCATION: (65309)..(65309)
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (36543)..(36543)
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LOCATION: (36636)...(36636)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c,
FRATURE:
                  NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51
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OCATION: (44905)..(44
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74.4%; Score 18.6; DB 20; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; G
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NAME/KEY: misc_feature
LOCATION: (152500) .(152500)
OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a,t,c, or
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NAME/KEY: misc_feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,t,c, or
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NAME/KEX: misc feature
LOCATION: (9921). (9921)
OTHER INFORMATION: n equals a,t,c, or
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NAME/KEY: misc feature
LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (145171). (145171)
OTHER INFORMATION: n equals a,t,c,
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MAME/KEY: misc_feature
LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals a,t,c,
                                                                         NAME/KEY: misc feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,t,c,
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ORGANISM: Haemophilus influenzae
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LOCATION: (152530)..(152530)
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LENGTH: 1830121
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us-09-544-776-4.rnpb

APPLICANT: MAI GENONICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: BATES, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: Holm, Tom
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APPLICANT: Hol ö ö Gaps Gaps Query Match 74.4%; Score 18.6; DB 22; Length 1830121; Best Local Similarity 64.0%; Pred. No. 2.1e+02; Matches 16; Conservative 5; Mismatches 4; Indels 0; G ö Length 564; Indels 73.6%; Score 18.4; DB 22; 70.0%; Pred. No. 1.2e+02; tive 5; Mismatches 1; 1071778 CAACTTCAGGATGCCCTTTATGCCC 1071754 1 CAACUUCAGGAUUCCAGAUAUGCCC 25 FEATURE:
NAME/KEY: misc feature
LOCATION: (150841). (150841)
FEATURE INFORMATION: n equals a,t,c, or NAME/KEY: misc feature LOCATION: (152500)..(152500) OTHER INFORMATION: n equals a,t,c, or ; Sequence 58889, Application US/10972079; Publication No. US20050153317A1; GENERAL INFORMATION: ö or NAME/KEY: misc_feature LOCATION: (145171). (145171) CTHER INFORMATION: n equals a,t,c, o FEATURE: NAME/KEY: misc_feature LOCATION: (145942). (145942) OTHER INFORMATION: n equals a,t,c, o ; TYPE: DNA ; ORGANISM: Chicken 19866894316535_1 US-10-972-079-58889 NAME/KEY: misc feature LOCATION: (147197)...(147197) OTHER INFORMATION: n equals a,t,c, RESULT 12
US-09-851-682A-2/c
'Sequence 2, Application US/09851682A
'Patent No. US20020091248A1
'GENERAL INFORMATION: LOCATION: (145058)..(145058) OTHER INFORMATION: n equals a,t,c, 318 TCAGGTTTCCAGATATGCCC 337 6 UCAGGAUUCCAGAUAUGCCC 25 14; Conservative Query Match Best Local Similarity US-10-972-079-58889 Matches à g ઠે g

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ORGANISM: Human
FEATURE:
                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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Publication No. US2005147987A1

SEQUENCE 312, APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT APPLICATION NUMBER: 60/231,397
PRIOR PILLING DATE: 2000-09-08

PRIOR FILLING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1543, Application US/10893315
Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00786
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                                                                             APPLICANT: Leng, Song

APPLICANT: Leng, Song

APPLICANT: Sheffield, Val

APPLICANT: Welefield, Val

APPLICANT: Welefield, Val

TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYP

TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF

FILE REFERENCE: 200130.442

CURRENT APPLICATION NUMBER: US/09/851,682A

CURRENT APPLICATION NUMBER: US/09/172,422

PRIOR FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PASESEQ for Windows Version 3.0

IENGTH: 8473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 9; Length 8473; Pred. No. 1.6e+02;
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65.0%; Pred. No. 1...
6; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 601
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Adams, Arwen E.
Chiu, Choi Ying
Duhl, David
                                                                Gorman, Susan W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.6
Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-893-315-1543/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-893-315-332/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-893-315-332
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Pred. No. 3.18+02;
4; Mismatches 0; Indels 0;
                                                                                                                                                                 Score 18; DB 22; Length 601;
Pred. No. 1.9e+02;
4; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 2172
SOFTWARE: FREESEQ FOR WINDOWS Version 4.0
SEO ID NO 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 30, 2005, 15:29:44
Job time : 490.108 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(117231)
; OTHER INFORMATION: n = A,T,C or G
US-10-893-315-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4257 CAACTTCAGGATTCCAGA 4240
                                                                                                                                                                                                                                         521 CAACTTCAGGATTCCAGA 504
                                                                                                                                                                                                                         1 CAACUUCAGGAUUCCAGA 18
                                                                                                                                                                    72.0%;
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAACUUCAGGAUUCCAGA
                                                                                                                                                                  Query Match 72.0
Best Local Similarity 77.8
Matches 14; Conservative
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July 30, 2005, 12:02:47 ; Search time 483.108 Seconds (without alignments) 334.933 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOOP_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7287783 seqs, 3236178273 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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			Description	Sequence 169389,	Sequence 7, Appli	Sequence 7, Appli	Sequence 23, Appl	Sequence 25, Appl	Sequence 27, Appl	Sequence 17, Appl
SUMMARIES			QI	100.0 25 21 US-10-956-157-169389	US-09-758-140-7	US-09-972-599A-7	US-09-972-599A-23	US-09-972-599A-25	US-09-972-599A-27	US-09-758-140-17
			ВВ	21	0	6	σ	6	σ	σ
			Match Length DB ID	25	75	75	75	90	105	120
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			Score	25	25	25	25	25	25	25
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RESULT 2

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Sequence 17, Appl Sequence 19, Appl	19,	e 10,	6	976	Sequence 3484, Ap	Sequence 163, App	Sequence 2, Appli	Sequence 110, App	Sequence 5, Appli	Sequence 156, App	Sequence 9762, Ap	Sequence 9763, Ap	Seguence 9765, Ap	Sequence 9766, Ap	Sequence 9767, Ap	Seguence 349, App	Sequence 4527, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 62, Appl	Sequence 1705, Ap	Sequence 10, Appl	10,	22,	4530	m	e	Sequence 4531, Ap	Sequence 54, Appl	382,	Sequence 4529, Ap	•	Sequence 1, Appli	Sequence 22, Appl	Sequence 212, App
9 US-09-972-599A-17 9 US-09-758-140-19	9 US-09-972-599A-19	19 US-10-327-213-10		21 US-10-956-157-9764	US-09-880-107-34		18 US-10-660-946-2	11 US-09-978-360A-110	9 US-09-789-386-5	14 US-10-175-523-156	21 US-10-956-157-9762	21 US-10-956-157-9763	21 US-10-956-157-9765	21 US-10-956-157-9766	21 US-10-956-157-9767	9 US-09-823-245A-349	21 US-10-956-157-4527	9 US-09-765-205-5	21 US-10-347-669-5	17 US-10-439-388-62	US-1	19 US-10-466-258-10	22 US-10-466-391A-10	17 US-10-220-891-22		19 US-10-466-258-3	22 US-10-466-391A-3	21 US-10-956-157-4531	14 US-10-060-036-54	18 US-10-641-643-382	21 US-10-956-157-4529	21 US-10-956-157-4528	9 US-09-789-386-1	9 US-09-893-348-22	18 US-10-267-502-212
120 198	198	198	261	9	639	668	799	994	1122	1160	1400	1400	1400	1400	1400	1514	1609	1610	1610	1785	1785	1798	1798	1980	2050	202	2052	2226	2235	2610	2883	3478	3579	3579	3579
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ALIGNMENTS

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Sequence 169389, Application US/10956157
; Sequence 169380, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; ATTLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT PILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SEQ ID NO 169389
; LENGTH: 25
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25 CTGGATAGCTTGGATCACACCCTTG 1
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Matches 18; Conserv
RESULT 1
US-10-956-157-169389/c
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US-09-758-140-7/c

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US-959/2-994-24)

US-959/2-994-24)

Sequence 23, Application US/09972599A

Patent No. US20020077295A1

GENERAL INFORMATION:

APPLICANT: STRITTWATER, STEPHEN M.

TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

FILE REPRESENCE: CO77 CIP US

CURRENT APPLICATION NUMBER: PCT/US01/01041

FRICA PAPLICATION NUMBER: PCT/US01/01041

FRICA FLING DATE: 2001-01-12

FRICA PAPLICATION NUMBER: 60/236,378

FRICA FLING DATE: 2000-09-29

FRICA FLING DATE: 2000-09-29

FRICA PAPLICATION NUMBER: 60/236,378

FRICA FLING DATE: 2000-09-29

FRICA RADICATION NUMBER: 60/175,707

FRICA RADICATION NUMBER: 60/175,707

FRICA RADICATION NUMBER: 60/175,707

FRICA RADICATION NOSE: 57

SOFTWARE: PARENT NOS: 57
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ORGANISM: Homo sapiens
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                                                                                                                  APPLICANT: Strittmatter, Stephen M.

TITLE OF INVENTION: No. US20020012965Alo Receptor-Mediated Blockade of Axonal Growth
FILE REPERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US/09/758,140
CURRENT FILING DATE: 2001-01-12
PRIOR PPLICATION NUMBER: US 60/175,707
PRIOR PILING DATE: 2000-01-12
PRIOR PPLICATION NUMBER: US 60/207,366
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,378
PRIOR PILING DATE: 2000-05-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 75
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| Sequence 7, Application US/0997259A
| Patent No. US20020077295A1
| GENERAL INFORMATION:
| APPLICANT: STRITTMATTER, STEPHEN M.
| APPLICANT: STRITTMATTER, STEPHEN M.
| TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
| FILE REFERENCE: C077 CIP US
| CURRENT FILING DATE: 2001-10-06
| PRIOR APPLICATION NUMBER: PCT/US01/01041
| PRIOR FILING DATE: 2001-01-12
| PRIOR FILING DATE: 2001-01-12
| PRIOR FILING DATE: 2001-01-12
| PRIOR FILING DATE: 2000-09-29
| PRIOR FILING DATE: 2000-09-29
| PRIOR FILING DATE: 2000-09-29
| PRIOR FILING DATE: 2000-01-12
| PRIOR FILING DATE: 2000-01-12
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| PRIOR FILING DATE: 2000-01-12
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| PRIOR FILING DATE: 2000-01-12
| PRIOR FILING DATE: 2000-01-12
| RECORD PRIOR FILING DATE: 2000-01-12
| SOUTWARE: PATENTIN VENER: PATENTIN VENE
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100.0%; Score 25; DB 9; Length 75;
Best Local Similarity 72.0%; Pred. No. 0.039;
Matches 18; Conservative 7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 CTGGATAGCTTGGATCACCCTTG 12
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Sequence 7, Application US/09758140
Patent No. US20020012965A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REPERBERGE. COT7 CIP US
CURRENT APPLICATION NUMBER: US/9/9/72,599A
CURRENT PILING DATE: 2001-10-06
PRIOR PILING DATE: 2001-01-12
PRIOR PLILOR DATE: 2001-01-12
PRIOR PLILOR DATE: 2001-01-12
PRIOR PLILOR DATE: 2000-01-12
PRIOR PLILOR DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-01-22
PRIOR PLING DATE: 2000-01-23
PRIOR PLING DATE: 2000-01-23
PRIOR PLING DATE: 2000-01-23
PRIOR PLING DATE: 2000-01-23
PRIOR PLING DATE: 2000-01-12
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PRIOR DATE: 2000-01-12
PRIOR DATE: 2000-01-12
PRIOR DATE: 2000-01-12
PRIOR DATE: 2000-01-12
PRIOR DATE: 2000-01-12
OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1079; OTHER INFORMATION: of human No. US20020077295AloA
US-09-972-599A-23
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OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1084
OTHER INFORMATION: of human No. US20020077295AloA
US-09-972-599A-25
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100.0%; Score 25; DB 9; Length 75;
Best Local Similarity 72.0%; Pred. No. 0.039;
Matches 18; Conservative 7; Mismatches 0; Indels
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1 CUGGAUAGCUUGGAUCACACCCUUG 25

36 CTGGATAGCTTGGATCACACCCTTG 12

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| Sequence 19, Application US/09758140
| Sequence 19, Application US/09758140
| Patent No. US20020012965A1
| GENERAL INFORMATION:
| APPLICANT: Stritmatter, Stephen M.
| TITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth
| FILE REPRENCE: 44574-5073-US
| CURRENT PILING DATE: 2001-01-12
| CURRENT PILING DATE: 2001-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-13
| PRIOR FILING DATE: 2000-09-26
| PRIOR FILING DATE: 2000-09-26
| PRIOR FILING DATE: 2000-09-29
| PRIOR FILING DATE: 2000-09-29
| SOFTWARE: Patentin Ver. 2.1
| SEQIID NO 19
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APPLICANT: STRITTMATTER, STEPHEN M.

TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
PILE REFERENCE: C077 CIP US
CURRENT APPLICATION NUMBER: US/09/972,599A
CURRENT FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-12
PRIOR PLICATION NUMBER: 09/758,140
PRIOR PLICATION NUMBER: 09/758,140
PRIOR PLICATION NUMBER: 06/236,378
PRIOR FILING DATE: 2000-01-12
PRIOR PLICATION NUMBER: 60/207,366
PRIOR PLICATION NUMBER: 60/207,366
PRIOR FILING DATE: 2000-05-29
PRIOR PLICATION NUMBER: 60/175,707
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
TENNORM 17
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OTHER INFORMATION: Description of Artificial Sequence: cDNA encoding
OTHER INFORMATION: receptor binding inhibitor Pep2-41
US-09-972-599A-17
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                                                                              Query Match 100.0%; Score 25; DB 9; Length 120; Best Local Similarity 72.0%; Pred. No. 0.042; Matches 18; Conservative 7; Mismatches 0; Indels
; OTHER INFORMATION: receptor binding inhibitor Pep2-41 US-09-758-140-17
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: No. US20020012955Alo Receptor-Mediated Blockade of Axonal Growth FILE REPERENCE: 44574-5073-008
CURRENT APPLICATION NUMBER: US 60/175,707
PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
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Sequence 27, Application US/09972599A

Sequence 27, Application US/09972599A

Sequence 27, Application US/09972599A

GENERAL INFORMATION:
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REFERENCE: C077 CIP US
CURRENT PILLING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: PCT/US01/01041

PRIOR PILLING DATE: 2001-01-12

PRIOR PILLING DATE: 2001-01-12

PRIOR PILLING DATE: 2000-09-29

PRIOR PILLING DATE: 2000-09-29

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-01-12

PRIOR PILLING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 57

SEQ ID NO 27

LENGTH 105
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US-09-972-599A-27
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                                                             Gaps
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100.0%; Score 25; DB 9; Length 105;
Best Local Similarity 72.0%; Pred. No. 0.041;
Matches 18; Conservative 7; Mismatches 0; Indels
  ; Score 25; DB 9; Length 90;
Pred. No. 0.04;
7; Mismatches 0; Indels
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  Query Match
Best Local Similarity 72.0%; F
Matches 18; Conservative 7;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-758-140-17/c
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COMPUTER READABLE FORM:
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COUNTRY: U.S.
ZIP: 94304
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
US-10-327-213-10
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LENGTH: 198
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                      FEATURE:

NAME/KRY: CDS

LOCATION: (1)..(198)

LOCATION: (1)..(198)

COP-1758-140-19

US-09-758-140-19
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CTHER INFORMATION: Full receptor binding region of No. US20020077295Alo gene
US-09-972-599A-19
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TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REFERENCE: 0077 CTP US
CURRENT APPLICATION NUMBER: US/09/972,599A
CURRENT FILING DATE: 2001-10-06
PRIOR PELICATION NUMBER: PCT/USO1/01041
PRIOR PELICATION NUMBER: 097758,140
PRIOR PILING DATE: 2001-01-12
PRIOR PELICATION NUMBER: 60/236,378
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,366
PRIOR PLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PALEGATION VUMBER: 61/15,707
PRIOR PLING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 19
LENGTH: 198
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Patent No. US20020077295A1

Patent No. US20020077295A1

GENERAL INFORMATION:

TITLE OF INVENTION: NGCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

FILE REFERENCE: C077 CIP US

CURRENT APPLICATION NUMBER: US/09/972,599A

CURRENT FILING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: PCT/US01/01041

PRIOR PLING DATE: 2001-01-12

PRIOR PLING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 09/759,140

PRIOR APPLICATION NUMBER: 60/759,140

PRIOR APPLICATION NUMBER: 60/236,378

PRIOR APPLICATION NUMBER: 60/236,378

PRIOR FILING DATE: 2000-09-29
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Best Local Similarity 72.0%
Matches 18; Conservative
                                                                                                                                                                                                                      18; Conservative
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ORGANISM: Homo sapiens
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Matches 18; Conserv
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APPLICANT: FILBIN, MARIE T.
APPLICANT: DOMENICONI, MARCO
APPLICANT: DOMENICONI, MARCO
APPLICANT: CAO, ZIXUAN
TITLE OF INVENTION: INHIBITORS OF WYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
FILE REFERENCE: CUNY/003
CURRENT APPLICATION NUMBER: US/10/327,213
CURRENT FILING DATE: 2002-12-20
KURBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                         ; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1120; OTHER INFORMATION: of human No. US20020077295AloA
US-09-972-599A-21
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Score 25; DB 19
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches
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PRIOR APPLICATION NUMBER: 60/207,366
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/175,707
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 21
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                  33 CTGGATAGCTTGGATCACACCCTTG 9
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US-10-327-213-10/c
US-10-327-213-10/c
Sequence 10, Application US/10327213
Publication No. US20040121341A1
GENERAL INFORMATION
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Gaps
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OTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023
NAME/KEY: unsure
LOCATION: (1).. (639)
OTHER INFORMATION: n = a or c or g or t
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Cockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3484

LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 9; Length 639; 72.0%; Pred. No. 0.052; tive 7; Mismatches 0; Indels
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Job time : 484:108 secs
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Matches 18; Conservative
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ORGANISM: Homo sapiens
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Pred. No. 0.046;
7; Mismatches 0; Indels
                                                                                                                                                  COMPUTER: IBM Compatible
OPERATIOS SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.10/660,946
FILING DATE: 12-Sep-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CUGGAUAGCUUGGAUCACACCCUUG 25
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 72.0%; Matches 18; Conservative 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: SPLNFET01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
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APPLICANT: Wyeth
APPLICANT: Wounte, William
APPLICANT: Mounte, William
APPLICANT: Mounte, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805

124 CTGGATAGCTTGGATCACACCCTTG 100

ò 셤 Sequence 9764, Application US/10956157 Publication No. US20050118625A1 GENERAL INFORMATION:

US-10-956-157-9764/c

RESULT 14

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Gaps ö

; Score 25; DB 21; Length 600; Pred. No. 0.051; 7; Mismatches 0; Indels (

Query Match
Best Local Similarity 72.0%;
Matches 18; Conservative 7

SOFTWARE: Patentin version 3.2 SEQ ID NO 9764 LENGTH: 600

TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-9764

216 CTGGATAGCTTGGATCACACCCTTG 192

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RESULT 15 US-09-880-107-3484/c ; Sequence 3484, Application US/09880107

1 CUGGAUAGCUUGGAUCACACCCUUG 25

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Sequence 4530, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
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                                                                                                                                                                                                                              (without alignments)
11092.639 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                    Description
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
                                                                                                                                                                                           August 1, 2005, 15:15:15 ; Search time 1307 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-10-956-157-4531
1 US-10-956-157-4530
9 US-10-466-258-3
2 US-10-466-391A-3
US-09-765-205-5
1 US-10-347-669-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Sequence 10, Appl Sequence 349, Appl Sequence 349, Appl Sequence 4527, Appl Sequence 9726, Appl Sequence 9767, Appl Sequence 9767, Appl Sequence 9767, Appl Sequence 9767, Appl Sequence 156, Appl Sequence 156, Appl Sequence 156, Appl Sequence 156, Appl Sequence 170, Appl Sequence
  US-10-466-258-10
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US-10-66-036-349
US-10-056-157-4527
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ALIGNMENTS

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0; Gaps
       Sequence 54, Application US/10060036

| Bublication No. US2030073144A1
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. |
| APPLICANT: Adale, Michael D. |
| APPLICANT: Persing, David H. |
| APPLICANT: Hopeway and H. |
| APPLICANT: Adale, Michael J. |
| APPLICANT: Persing, David H. |
| APPLICANT: Adale, Michael J. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Adale, Michael J. |
| APPLICANT: PERSING, COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| FILE REFERENCE: 210121.566 |
| CURRENT APPLICATION NUMBER: US/10/060,036 |
| CURRENT FILING DATE: 2002-01-30 |
| NUMBER OF SEQ ID NOS: 4560 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 54 |
| LENGTH 2335 |
| TENGTH 2335 |
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2231; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54
US-10-060-036-54
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CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGCCCAGCCCTCTCAGTCCTCCCCAACCC

Oy 2221 TAAAAAAAA 2231 Db 2225 TAAAAAAAA 2235	ko qa	CGCCCAAGCGCAGGGCTCCTCGGGCTCAGAGGTTGTTGACCTCCTGTACTGGAGAGACA 7
RESULT 2 US-10-956-157-4531 ; Sequence 4531, Application US/10956157 ; Publication No. US20050118625A1 ; APPLICANT: Wyeth	8 & 8 &	721 TTAAGAAGACTGGAGTGGTGTTTGGTGCCTGTTTCCTGCTGTTTTATAGAGATAT 780 725 TTAAGAAGACTGGAGTGTTTGGTGCCGGCCTATTCCTGCTGCTTTCATTGAGAGTAT 784 726 TTAAGAAGACTGGAGTGTTTGGTGCCGGCCTATTCCTGCTGCTTTCATTGAGAGTAT 784 781 TCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGGTGACCATCAGCT 840 785 TCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCTGCTCTGTGACCATCAGCT 844
; APPLICANT: Mounts, William ; TITLE OF INVENTION: NUCLEIC ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES ; FILE REFERENCE: 031896-043000 (AM 101081)	\$ 68	841 TTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 900
CURRENT FILING NOMES: 05/10/956,15/ ; CURRENT FILING DATE: 2004-10-04 ; NUMBER OF SEQ ID NOS: 319805 ; SOFTWARE: Patentin version 3.2	& 8	901 GGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATT 960
; SEQ 1D NO 4531 ; LENGTH: 2226 ; TYPE: DNA TYPE: TOO SADISH HOMO SADIEDS	ò 8	961 CTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATG 1020
Query Match Query Match Query Match Guery Match Best Local Similarity 99.7%; Precd. No. 0; Matches 2218; Conservative 0; Mismatches 0; Indels 7; Gaps 2;	<i>≿</i> 8	
AGTAGGTCCCTCGAGTCAGCCCAGCCCTCTCAGTCGTCCCCAACCC 60 ALTHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	충 옵	
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181 GCCCACCCGGCGCGCGCTTCAAGTACCAGTTCGTGAGGAGCCCGAGGAGGAGGGGGGGG	පි සි	132
241 AGGAAGAAGAGGAGGAAGAGAGACGACGAGACGAAGACCTGAGGAGCTGCAGGTGC 245 AGGAAGAAGAGAAGAGAAGAGACAAGACGACGAAGAAGACTGCAGAGAGAG	<i>∂</i> 8	
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Qy 361 GCGCGCCCTGATGGACTTCGGAAATGACTTCGTGCCGCCGGGCGCCCCGGGGACCCCTGC 420 Db 365 GCGCCCCTGATGGACTTCGGAAATGACTTCGTGCCGCCGGGCGCCCCGGGGACCCCTGC 424	୪ ଶ ୍	TTCATCATCATAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATTT 15
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Qy 541 Agancandadccrcccdaccrccagaccrcccccaga 600 Db 545 Agancandadccrccccccagaccrccccccccccccaga 600	<i>ò</i>	CCCTTTCAGTTTGTGCACTGTGTATGGTCGTGTAGATTGATGCAGATTTTCTGAAATG 167 CCCTTTTCAGTTTGTGCACTGTGTGGTCCGTGTAGATTGATGCAGATTTTCTGAATG 168
Qy 601 cagaseccensus 600	λό q _α	1677 AARIGITTGITTRACGROATCAIRCCGGTAAGGAGARIGACAAAGCTIGCITTICIG 1/36
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CATGTGAACTGCACGATAAAGGAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGAT 1031
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                                                                                                                                                                                                                                          CCGCAGCCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGACGAAGAAGAG
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                                                                               Score 1892.8;
Pred. No. 0;
0; Mismatches
                                                                               Query Match
Best Local Similarity 94.8%;
Matches 2044; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
                                ; NAME/KEY: CDS
; LOCATION: (67)..(1188)
US-10-466-258-3
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Publication No. US20040132096A1
GENERAL INFORMATION:
TITLE OF INVENTION: ASSAY
TITLE OF INVENTION: ASSAY
CURRENT APPLICATION WHMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEROID NO 3.0
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                                                                                                                                                                                                                                                                          Sequence 3, Application US/10466391A
Publication No. US20040146953A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REPERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,391A
CURRENT PILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3.
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Pred. No. 0;
0; Mismatches
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ORGANISM: Homo sapiens
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US-10-466-391A-3
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NAME/KEY: CDS
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RESULT 9 US-10-466-391A-10

Sequence 10, Application US/10466391A
Publication No. US20040146953A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW

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Sequence 4532, Application US/10956157

Publication No. US20050118625A1

Publication No. US20050118625A1

Fubblication No. US20050118625A1

GENERAL INNORMATION:

APPLICANT: Wounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: UNMER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARRE: PALENTIN VERSION 3.2

SEQ ID NO 4532
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                                                                                                                                                                                   Sequence 3766, Application US/10956157
Publication No. US20050118625A1
Publication No. US20050118625A1
Publication No. US20050118625A1
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: NUMBER: US/10/956,157
CURRENT PAPLICATION UNDBER: US/10/956,157
CURRENT PAPLICATION UNDBER: US/10/956,157
CURRENT PAPLICA 100 NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 9766
LENGTH: 1400
 2187
                           1516 GATTTATACCATTGTGGTTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACT 1575
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GATTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACT
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Pred. No. 0;
0; Mismatches
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Matches 1396; Conservative 0
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; ORGANISM: Homo sapiens
US-10-956-157-9766
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US-10-956-157-9766
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         4054 IGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTTTAGACGAGATCATACCGGTAA
                                                                 4114 AGCAGGAATGACAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGT
                                                                                                                    CIGTITICAACAIGAAAIGCCACACACAIAGAACTICCAACAACAICAAITICAIIGGACA
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1649 TGTAGATTGAGAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAA
                                                                                                       1889 ACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGAATATTTCTAGGAGCACTACCAT
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APPLICANT: Olsen, Nancy J
TITLE OF INVENTION: Method for Predicting Autoimmune Disease
TITLE REFERENCE: 1242/68
CURRENT APPLICATION NUMBER: US/10/439,388
CURRENT FILING DATE: 2003-05-16
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
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Best Local Similarity 99.1%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches
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; Publication No. US20030228617A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-439-388-62
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                                                                                                                                   GTTGTTGACCTCCTGTACTGGGAGACATTAAGAAGACTGGAGTGGTTTGGTGCCAGC
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                                                                                                                     GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTTTTGGTGCCAGC
                                                                                           67;
                                                            Query Match
61.1%; Score 1369; DB 21; Length 4623;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1466; Conservative 0; Mismatches 0; Indels 67;
                                                                                        0; Mismatches
           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4532
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Db 1446 ATGTGTAGTTCCAAAGCACATAAGCTAGAAA Qy 1951 GTTTTCAACATGAAATGCCACACACACATAGAA Db 1506 GTTTTCAACATGAAATGCCACACACACATAGAA	Oy 2011 CTGACTGTAGTTAATTTTGTCACAGAATCTA	Search completed: August 1, 2005, 20:25:49 Job time : 1318 secs													
812 CTTGGCCTGCTCTGTGACCATCAGGTTAGGATATACAAGGGTGTGATCCAAGCTAT 871 871 871 871 871 872 873 874 875		1052 GATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC 1111 	1112 TCTCATTTCACTCTTCAGTGTTCTGTTATTATGAACGGCATCAGGCACAGATAGAT	1172 TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAT 1231 	1232 CCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTCATCT 1291 	1292 TTAAAGGGATATTCATTTGATTATACGGGGGAGGGTCAGGAAACAAAC	1352 TGCAGTGCAGTTTCACACATGTTGTTACATCTTTATTTTTAGCCATGCACTGTTGTGGG 1411 	1412 GAAAAATTACCTGTCTTGACTGCCATGTCTTCATCATCATAAGTATTGTAAGCTGCTATG 1471 	1472 TATGGATTTAAACCGTAATCATATCTTTTCCTATCTGAGGCACTGGTGGAATAAAAAC 1531 	1532 CTGTATATTTTACTTTGTAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGT 1591 	1592 GGAGCTAG-AAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTATGGTCCGTG 1650 	1651 TAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAG 1710 	1711 CAGGAATGACAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTA 1770 	1771 TATTAATTGCCAATATAAGTAAATATAGATTATATATGTATAGTGTTTCACAAAGGTTAG 1830 	1831 ACCTTTACCTTCCAGCCACCCCACAGTGCTTGATATTCAGAGTCAGTC

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Best Local Similarity 99.3
Matches 1539; Conservative
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ORGANISM: Homo sapiens
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Sequence 3253, Ap
Sequence 382, App
Sequence 14995, A
Sequence 1339, Ap
Sequence 11204, A
Sequence 11204, A
Sequence 741, App
Sequence 741, App
Sequence 2727, App
Sequence 279, App
                                                                     1, 2005, 11:22:53; Search time 392 Seconds (without alignments) 9350.153 Million cell updates/sec
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                                                                                                                                   Description
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
          5.1.6
Compugen Ltd.
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US-08-700-607-2
US-09-513-999C-10680
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-09-949-016-1127
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US-09-949-016-2988
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                                                                                                                                                                                       1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
          GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
                                                                                                                                                        IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                               US-09-544-776-1
2240
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Match Length
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Perfect score:
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Maximum
                                                                       Run on:
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No.
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
NAME/KEY: unsure
LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
OTHER INFORMATION: a, t, c, g, or other
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                                                                                                                                                                         Sequence 1419, Ap
Sequence 1419, Ap
Sequence 3784, Ap
Sequence 100, App
Sequence 100, App
Sequence 100, App
Sequence 15051, A
Sequence 12869, A
Sequence 4018, A
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11198, A
9, Appli
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Sequence 1
Sequence 5
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US-08-700-607-4
US-09-949-016-117588
US-09-949-016-117589
US-09-799-451-111
US-09-513-999C-11198
US-09-149-476-192
US-09-149-476-192
US-09-506-729-51
US-09-5949-016-1419
US-09-513-999C-3784
US-09-513-999C-3784
US-09-513-999C-3784
US-09-949-016-14730
US-09-949-016-12869
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99.3%; Pred. No. 0;
iive 0; Mismatches
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APPLICANT: JOLKMULM, WAYNE
APPLICANT: WOLKMULM, WAYNE
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PE-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT PELLING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-484-970B-106; Sequence 106, Application US/09484970B; Sequence 106, Application US/09484970B; CENERAL INFORMATION:
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Sequence 3253, Application US/09949016

Batent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: (0/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3253
LEMOTH: 1669
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CCTATTCCTGCTGCTGCTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC
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                                                      TTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTA
                                                                          4708 TIATACCATIGIGGTTTAAGCIGTACTGAACTAAATCTGTGGAATGCATIGTGAACTGTA
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                                                                                                                             AAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAANGNNANNAGNGAAAA 4817
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99.7%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity
Matches 1419; Conserv
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US-09-949-016-3253
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                    4648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2011 CIGACIGIAGIIAAITITGICACAGAAICIAIGGACIGAAICIAAIGCIICCAAAAAIGI 2070
                                                                                                                                                                                                                   TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 1232
                                                                                                                                                                                                                                                     3748 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 3807
                                                                                                                                                                                                                                                                                                           3808 CCTGGATTGAAGCGCAAAGCTGAATGAAAAGGCCCAAAATAATTAGTAGGAGTTCATCTT 3867
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGG 1412
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                                                                                             3628 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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                                                                         ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT
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FOR THE DETECTION OF BLOOD CELL
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                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.4%; Pred. No. 2.6e-255;
Matches 1172; Conservative 0; Mismatches 10;
TITLE OF INVENTION: COMPOSITION FOR THE TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: 1708 FIARMACEUTICALS, IN STREET: 3174 FORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA ZIP: 94304
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAWE: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCS/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT14
CLONE: 1508778
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| Patent No. 6607879
| GENERAL INFORMATION:
| APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
| APPLICANT: Jeffrey J. Seilhamer
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Query Match
Best Local Similarity 97.9%;
Matches 1021; Conservative
j LENGTH: 42075j TYPE: DNAj ORGANISM: HumanUS-09-949-016-14995
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Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS(
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS(
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF I
FILE REFERENCE: CLOOJ307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-06
PRIOR FILING DATE: 2000-06
PRIOR FILING DATE: 2000-06
SPRIOR PRIOR FILING DATE: 2000-06
SPRIOR PRIOR FILING DATE: 2000-06
SPRIOR PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-949-016-14995
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                                                          1189 ATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCA
                                                                                                                      AAGCTGAATGAAAACGCCCCAAAATAATTAGTAGGAGTTCATCTTTAAAGGGGGATATTCAT
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                                Gaps
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 Length 42075
Score 996.2; DB 4; Length
Pred. No. 5e-230;
0; Mismatches 18; Indels
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1732 TTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATTAATTGCCAATATAAGTA 1791
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                                                                                                   992 GGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT 1051
                                        647 CCCTGGATTGAAGCGCAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGAGTTCATCT 706
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                                                                                                                                                                                                            GAFGIGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC
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APPLICANT: Jobert, S.
APPLICANT: Glocdano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3839
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99.4%; Pred. No. 4.1e-116;
iive 0; Mismatches 0;
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Best Local Similarity 99.4
Matches 534; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 3..224
US-09-621-976-3839
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APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES:

ADDRESSEDE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 682; DB 2; I
Pred. No. 5.4e-155;
0; Mismatches 0;
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBW Compatible
COMPUTER: IBW Compatible
COMPUTER: IBW Compatible
SOFTWARE: FeatSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                        40169 ATAAAGCTTATAGACTTAAAATA 40191
                                                                              2205 ATAAAGCTTATAGACTTAAAAAA 2227
                                                                                                                                                                                RESULT 5
US-08-700-607-2
; Sequence 2, Application US/08700607
; Patent No. 5858708
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 99.9%;
Matches 693; Conservative
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US-08-700-607-2
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                     GTGTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCCCACAGTGCTTGATATTTCAGA
                                                                                241 GTCAGTCATTGGTTATACATGTGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGAAGAAGAATATTT
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Sequence 3840, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Obbert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 3840

LENGTH: 508
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Pred. No. 1.1e-106;
0; Mismatches 0;
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Best Local Similarity 99.4%;
Matches 495; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 3..224
US-09-621-976-3840
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CACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTGTTGCAAAGCACAT 1911
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                                                                                           241 AAGCTAGAAGAAGAAATTTCTAGGAGCACTACCATCTGTTTCAACATGAAATGCCAC
                                     CACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTGTAGTTCCAAAGCACAT
                                                                                                                                                  301 ACACATAGAACTC---CAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTC
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APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10680
LENGTH. 537
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PREEDI NO. 6783961,
GENERAL INFORMATION:
APPLICANT: Dumag Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 536
OTHER INFORMATION: r=a or g
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: 358
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US-09-513-999C-10680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

Patent No. 6783961

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INFORMATION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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15.3%; Score 343; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 343; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2227
                                                                                                                                                                                       Sequence 2227, Application US/09513999C
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                        1609 AA 1610
                                                                     495 AA 496
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; LOCATION: 236...
US-09-513-999C-2227
                                                                                                                                                                 JS-09-513-999C-2227
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US-09-621-976-741
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                                            2032 ACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGCAAATATGAAA 2091
                                                                                                                                          CATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGC 2151
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ACACATAGAACTC---CAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTC 357
                                                                          255 GATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTT
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961

FILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 11204

LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11204, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: n=a, g, c or t
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                                                                                                                                                                                                                                                                                     TGTACTGAACTAAATCTG 495
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Sequence 3309, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 05/09/949,016

CURRENT PELING DATE: 2000-00-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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                                                              92 cercaccacadraderecercescreaeresecendesecentricaerecedededate
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12.1%; Score 270.4; DB 4; Length
Best Local Similarity 67.3%; Pred. No. 4.4e-55;
Matches 382; Conservative 0; Mismatches 186; Indels
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; ORGANISM: Human
US-09-949-016-3309
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US-09-949-016-3309
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LENGTH: 2069
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                                                                                                                                                                                                                                                                                                                                                                                                                                      159
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                                                                                                                                                                                                                                                                                                    14.1%; Score 316.6; DB 4; Length 463; 88.9%; Pred. No. 1.2e-66; tive 11; Mismatches 0; Indels 33
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14.1%; Score 316; DB 4; Length 454;
Best Local Similarity 89.1%; Pred. No. 1.6e-66;
Matches 353; Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 740, Application US/09621976
; Sequence 740, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Johert, S. APPLICANT: Johert, J.Y.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET: OS4PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 GCGCCCCCTGATGGACTTCGGAAATGACTTCGTGCM 463
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                                                                                                                                                 NAME/KEY: CDS
| LOCATION: 237..461
| NAME/KEY: misc_feature
| LOCATION: 20
| COTHER INFORMATION: n=a, g, c or t
US-09-621-976-741
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 741
LENGTH: 463
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 88.99
Matches 353; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: 229..453
US-09-621-976-740
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US-09-621-976-740
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                                                                                   GAACTCAGGCCCCTCTTCTTAGTTGATGATTTAGTTCATCTCTGAAGTTTGCAGTGTTG 1052
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Matcher, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Renger, Gary
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APPLICANT: Renger, Gary
APPLICANT: Renger, Gary
APPLICANT: Bay, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: 1999-11-12
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 279
LENGTH: 301
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Patent No. 6329505
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| LOCATION: (1)...(301)
| OTHER INFORMATION: n = A,T,C or
US-09-439-313-279
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ORGANISM: Homo sapien
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-0-08
PRIOR FILING DATE: 2000-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREEEQ for Windows Version 4.0
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          CAGAAAACCGACGAAGGCCACCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCTTTCT 993
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Pred. No. 5.7e-55;
0; Mismatches 186; Indels 0;
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Best Local Similarity 67.3%;
Matches 382; Conservative 0
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Search completed: August 1, 2005, 18:14:51 Job time : 395 sec8
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1533 68.4 4060 9 AY123250 1533 68.4 4070 9 AY122249 1533 68.4 4102 9 AY123245 1533 68.4 4109 9 AY122248 1533 68.4 4109 9 AY122248	1533 68.4 4789 6 CQ874017 CQ874017 Seque 1533 68.4 4789 9 AY102279 AX220865 AR220865 Seque 1512 67.5 1691 9 AR132048 Homo	31 1467 65.5 1485 9 BC01073	1122 50.1 1122 6 bD249448 1122 50.1 1122 9 HSA251384 1097.6 49.0 2610 6 AR378937 1090.8 48.7 2410 10 BC070879 1072 47.9 2256 10 AF132046	1057 47.2 2782 6 AX7 1057 47.2 2782 10 AX 1057 47.2 2782 10 AF 1044.4 46.6 2209 10 AX	RESULT 1 APT48538 LOCUS LOCUS DEFINITION Homo sapiens reticulon 4b mRNA, complete cds. ACCESSION AF148538 VERSION AF148538 KEYWORDS KEYWORDS SOURCE Homo sapiens (human)	ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2235) AUTHORS Yang, J., Yu, L., Bi, A. D. and Zhao, S.Y. TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome	2014>2p13 by radiation hybrid mapping JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000) C. Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000) MEDLINE 20231542 PUBMED 10773680 REPERBNE 2 (Dasses 1 to 2235)	Direct Submission Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of Constite Budan Interestry No. 220 Handan Rd. Shanchai 200433.	iers sapiens" :9606" :19606" :1001 4b" G12177.1" G12177.1" PARGISARAVENTS PARGISARAVENTS PARGISARAVICA INDILYKGVIQAI ANKNYKDAWAKI
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.	5, 10:33	i-1 jtaggtccttaaaaaaaaaaaaaaaaaaaa 2240 Gapext 1.0	24227607955 residues ng chosen parameters: 9416466	0000 1 00% 1 100% 1 45 summaries			or of results predicted by chance to have a equal to the score of the result being printed, ysis of the total score distribution. SUMMARIES	DB ID Description	9 AF148538 AF148538 Homo sapi 9 AY102277 AY102277 Homo sapi 9 AY102278 AY102277 Homo sapi 9 AY102278 Homo sapi 9 AY102278 Homo sapi 9 AY102278 Homo sapi 9 BC068991 BC068991 Homo sapi 9 BC068991 BC068991 Homo sapi 9 BC026788 Homo sapi 9 AX129806 Homo sapi 6 CO783030 CO781019 6 CO783030 CO781010 6 CO783030 CO781010 6 CO769577 CO765577 7 AR040463 Homo sapi 9 BC016165 Homo sapi 9 BC016165 Homo sapi 9 BC016165 Homo sapi 9 BC014366 Homo sapi 9 BC014366 Homo sapi 9 AX10276 Homo sapi
Gopyright (c	non: August 1, 20	Title: Perfect gcore: 2240 Sequence: 1 cgtcaccacagtaggtcct Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.	d: 4708233 segs, umber of hits satisfyin	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 10 Maximum Match 10 Listing first 45	Database : GenEmbl:* 1: 9b ba:* 2: 9b_htg:* 3: 9b_in:* 4: 9b_om:* 5: 9b ow:* 7: 9b_pat:* 9: 9b_pi:*	04064	Pred. No. is the number of score greater than or equa and is derived by analysis	ery tch Length	1 2231 99.6 2235 3 2189 97.7 2276 4 2158 96.3 2332 5 1892.8 84.5 2052 6 1615 72.1 1728 7 1607.4 71.8 1610 10 1591.2 71.4 1619 11 1586.4 70.8 1694 12 1586.4 70.8 1694 13 1586.4 70.8 1694 14 1577.4 70.8 1694 15 1577.4 70.8 1694 17 1586.4 70.8 1694 18 1537.4 70.3 1709 16 1549 69.2 1700 17 1548 69.1 1784 18 1536.4 68.5 1800

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/gene="RTN4"
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LGHVNCTIKELRLFLVVDDLVDSLKFAVLAMVFTYVGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKLQAKIPGLKRKRE"
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2045 ATGGACTGAATCTAATGCTTCCAAAATGTTGTTTGTTTGCAAATATCAAACATTGTTAT 2104
                                                                                                                                                                                          CTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACT 2220
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EDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPARGPLVAP
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J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2332)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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Direct Submitssion

Submitted (07-MX-2002) Brain Research Institute, University

Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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/gene="RTN4"
/note="NOGO-B; RTN4-B1; alternatively spliced"
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/protein id="AAM64246.1"
/db xref="G1:26800562"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
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/evidence=experimental
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Van der Putten, H.
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Unpublished
2 (bases 1 to 2276)
Ito,T. and Schwartz,S.M.
Direct Submission
Submitted (27-FEB-1999) Pathology, University of Washington, 1959
Pacific NB, Seattle, WA 98195, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2276)
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180. .1301
/note="member reticulon gene family"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2389)
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Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
Location/Qualifiers
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Oerlle, T. and Schwab, M.E.
Direct Submission
Submitted (07-MX-2002) Brain Research Institute, University
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
                                                                                                                 Oertle, T., Huber, C., van der Putten, H. and Schwab, M.B. Genomic structure and functional characterisation of the of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
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97.5%; Pred. No. 0;
iive 0; Mismatches
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Van der Putten, H.
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
EC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Faika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angalique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, J., Smallus, D.B., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length munan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                    Submitted (05-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="Vector: pOTB7"
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Contact: MGC help desk
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Strausberg, R.
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Length 1728;

Score 1615; DB 9; I Pred. No. 3.4e-270;

72.1%; S 100.0%;

Query Match Best Local Similarity

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TTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 1011
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99.9%;
                         Query Match
Best Local Similarity 99.9
Matches 1608; Conservative
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                                       1192 IGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTA 1251
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Lin, H. and Cao, L.
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                                                                  TTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTA
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Bone marrow secreted proteins and polynucleotides.
BD231889
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C12N15/00, A61K37/02, C12N5/00
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002511231-A/3.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Ggapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: h Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
This clone has the following problem: The cds is short compared the longest cds in the locus.

Location/Qualifiers

1. 1668
                                                                                                                                                                                                         Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGCCCAGCCCTCTCAGTCCTCCCCAACCC
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                     human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/tissue type="Ovary, adenocarcinoma"
/clone_lib="NIH MGC_66"
/lab.host="DH106"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.5%; Score 1601; DB 9;
99.8%; Pred. No. 9.1e-268;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                    2 (bases 1 to 1668)
Strausberg, R.
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Matches 1615; Conservative
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                                   TTGATTCTCTGAAGFTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTA 1086
                                                                    1147 AACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATG 1206
                                                                                                                                                                                                                                                                                                                                                        AACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATG 1200
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                       CAAAATAATTAGTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGG
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61 CCACAACCGCCGCGGGCTCTGAGACGCGCCGGGGGGCGCGGCAGCTGCAGCTT	

According Acco			BC012619 BC012619 BC012619 Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone IMAGE:4082756), complete cds. IMAGE:4082756), complete cds. BC012619 BC012619 BC012619 BC012619 BC012619 Homo sapiens Homo sapiens Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo. Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo. Risausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Strausberg, R.L., Teingold, E.A., Grouse, L.H., Schaefer, C.E., Bhat, N.K., Hopkins, R.F., Joedan, H., Moore, T., Max, S.I., Wang, J., Hateh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McEwan, P.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, R.J., Hulyk, S.W., Villalon, D.K., Muting, M., Madan, A., Young, A.C., Shevchenko, Y., Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Banchez, A., Whiting, M., Touchman, J.W., Green, E.D., Bolfkard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
//Lone lib=lb(") Local Sillarity 100.04; Pred. No. 2e-267; Indels 0; Gaps 15: 19: Conservative 0; Minatch 100.04; Pred. No. 2e-267; Indels 0; Gaps 15: 19: Conservative 0; Minatch 100.04; Pred. No. 2e-267; Indels 0; Gaps 10: Conservative 0; Minatch 10: O; Minat	8 8 8 8 8 8	8 6 8 6 8 6 8 6 8 6 8 6	RESULT 10 BC012619 LOCUS DEFINITIC ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANIE REFERENCE AUTHORS
//Lone lib=lnkC* //Local Sillarity 100.04; Press 1899; DB 9; Length 1619; Local Sillarity 100.04; Press 1899; DB 9; Length 1619; Local Sillarity 100.04; Press 1800; DB 9; Length 1619; Local Sillarity 100.04; Press 1800; DB 9; Length 1619; Local Correct Conservative Co. 7. Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Mismatches 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Mismatches 0, Indels 0; Mismatches 0, Indels 0; Gaps 100:000; Mismatches 0, Indels 0; Mismatches 0; Mis	. 0 0 0 4		20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	/clone_lib="DMC" /note="cloning vector: pME18SFL3" /note="cloning vector: pME18SFL3" Local Similarity 100.0%; Pred. No. 2e-267; hes 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 1 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGCCCAGCCCTCTCAGTCCTCCCCAACCC	ATCTCCACCCTCCAGCCATGAAACCCCCCCCCCCCCCCC	AGGACAACGAGCCTCCGGCCCCCCCCCCCCCGGCCAGGAGCCCCCGGGGAGCCCCCGGGGAGCCCCCC

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 1477932 (Dasses 1 to 1654) 2 (Dasses 1 to 1654) 2 (Dasses 1 to 1654) 2 (Dasses 1 to 1654) 3 (Dasses 1 to 1654) 3 (Dasses 1 to 1654) 4 (Dasses 2 (Dasses 2 (Dasses 2 (Dasses 2 (Dasses 3 (Dasses	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: d Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2441932 This clone has the following problem: The cds is short compared to the longest cds in the locus. RESS Location/Qualifiers Source	/gene="RTN4" // db xref="MIN:604475" /db xref="MIN:604475" /db xref="MIN:604475" /db xref="LocusID:57142" /db xref="LocusID:57142" /db xref="LocusID:57142" /gene="RTN4" /codon_start=1 /product="reficion 4, isoform B" /product="refi
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                                                                                                Length 1694;
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Pred. No. 3.1e-265;
0; Mismatches 1;
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/mol_type="genomic DNA"
/db xref="taxon:9606"
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JP 2002017375-A/2868
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea 1 to 1694)
Ota, T., Niehikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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                                                1175 TTGTTTAATGGTCTGACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT
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                TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT
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                                                                                 1140 ATTTATGAACGCCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT
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Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2868 22-JAN-2002;
HELIX RESERVET INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2868
C3-JAN-2002
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JP 2002017375-A/2868.
Homo sapiens (human)
Homo sapiens
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SHINICHI KOJIMA
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JOURNAL
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Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Ton Ton Institute of Medical Science, University of Ton Ton Institute of Medical Science, University of Ton Ton Institute of Medical Science, University of Science Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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/replace=""
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/organism="Homo sapiens"
/mol_type="mixNa"
/mol_type="mixNa"
/db_xref="taxon:9606"
/clone="0VARC1001030"
/fissue_type="vary, tumor tissue"
/clone_lib="0VARC1"
/note="cloning vector: pME18SFL3"
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Pred. No. 3.1e-265;
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Isogai, T. and Otsuki, T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarau, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                      TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT
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AK075039
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Medical Genetics; Yamadacka 2-2, Suita, Osaka 567-0871, Jar
(E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
Fax:+81-6-6879-3369)
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                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tagami, S., Eguchi, Y., Kinoshita, M., Takeda, M. and Tsujimoto, Y. A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity Oncogene 19 (50), 5736-5746 (2000)
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Bguchi,Y.. Tagami,S. and Tsujimoto,Y.
Bjirct Submission
Submisted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Biomedical Research Center, Department of
                                                                                    TGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACT
                                                                                                                                                                           TGCAGTGTTGATGTGGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGTACT
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Search completed: August 1, 2005, 18:08:12 Job time: 9336 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aac64406 Human Nog	Abv94681 Human pan	Abk90133 DNA encod	Aaz36230 cDNA enco	Aak94408 Human ful	Adl31137 Full leng	Aaf32725 Human sec	Adi62860 Human apo	Adr83534 Human ret	Abs70449 Human bon	Abk90135 DNA encod	Abk34580 Human cDN	Aad08386 Human sec	Abv94680 Human pan	Adg32772 Human DNA	Adk14166 Human aut	Abx34563 Human mdd	Aba05903 Human RTN	Aaz56888 Human MAG	Aaf90325 Human NOG
SUMMARIES	a ID	3 AAC64406	5 ABV94681	5 ABK90133	3 AAZ36230	4 AAK94408	12 ADL31137	4 AAF32725	10 ADI62860	13 ADR83534	6 ABS70449	6 ABK90135	6 ABK34580	4 AAD08386	6 ABV94680	10 ADG32772	12 ADK14166	8 ABX34563	6 ABA05903	3 AAZ56888	4 AAF90325
	* Query Match Length DB	2240	2235	2052	1610	1694	1694	1758	1599	4789	4822	1798	1514	1683	4632	4632	1785	4698	1216	1122	1122
	% Query Match	6.66	9.66	84.5	71.8	70.8	70.8	70.6	70.4	68.4	68.1	66.5	65.8	65.4	62.9	65.9	60.7	59.2	54.3	50.1	50.1
	Score	2238.4	2231	1892.8	1607.4	1586.4	1586.4	1581	1577.4	1533	1525.2	1488.8	1473.4	1464.6	1409	1409	1359.2	1325	1216	1122	1122
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cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and callular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antegonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B
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ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ATCTCCACCCTCCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACA 180
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                                                                                                                                                                                                                                            99.6%; Score 2231; DB 6; Length 2235; 100.0%; Pred. No. 0; Namatches 0; Indels 0
                                                                                                                                                                                                               Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Matches 2231; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
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cytostatic; tumour; gene; ss
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P-PSDB; ABP68601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoB; Nogo-associated disease; metastasis; gene; ds.
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               ATGGACTGAATCTAATGCTTCCAAAATGTTGTTTGTTTGCAAATATCAAACATTGTTAT
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(SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                     CTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATG
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EACE polypeptides capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nego or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury. Stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, curvolation) injuries, such as spinal or head injury stroke, corresponding the projection of disportive disporders (e.g. pripheral nerve damage, and in neoplastic (e.g. glioblastomas, curvolation) in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polymoleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present nucleic acid sequence encodes the human NogoB protein of the invention 191 120 251 180 311 240 371 300 431 360 491 420 480 611 131 551 9 GAGGAGGAAGGAGGACGACGACGAACCTGCAGGAGCTGCAGGTGCTGCAGAAG GCGGCTCTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATCTCCACCCT CCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCCGG CCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCGG CCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGAGGAGGAAGAAGAG 121 CCGCAGCCCGCGTTCCAAGTACCAGTTCGTGAGGAGCCCGAGGACGAGGAAGAAGAGAG GAGGAGGAAGAGGACGACGACGACGACCTCGAGGAGCTGGAGGTGCTGGAGAGGAAG CCCGCCGCCGCCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGCGGCGCGCCCCTG 241 CCCGCCGCCGGGCTGTCCGCGCCCCCAGTGCCCACCGCCCCTGCCGCCGCCGGCGCCCCTG CCCGTCGCCCCGGAGCGCCGTGTTGGGACCCCGAGCCCGGTGTCGTCGACCCCC GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTTCAAGCTCCCTGAGGACGAG GCGCCATCCCCGCTGTCTGCCGCAGTCTCGCCCTCCAAGCTCCCTCAGGACGACGAG CCTCCGGCCCCGGCCTCCCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGAACCCGAGCCCGGTGTCGTCGACCGTGCCC 2; Indels 110; Gaps 84.5%; Score 1892.8; DB 6; Length 2052; 94.8%; Pred. No. 0; Sequence 2052 BP; 511 A; 512 C; 506 G; 523 T; 0 U; 0 Other; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 94.8
Matches 2044; Conservative 132 72 61 192 252 181 312 372 432 361 492 421 552 88888888888888888888888888888 Š 윱 ద 셤 ద 요 엄 ઠે 셤 8 셤 ò 음 8 8 ò ठ 8

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1151 CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1140 1331 TAATTAGTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAG 1260 1380 1567 1091 961 TCTCTGAAGTTTGCAGTGTTGATGTGGGGGTATTTACCTATGTTGGTGCCTTCTTTAATGGT 1020 CIGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGG 1080 AAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTC----CTATC 1507 CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTGGAT 1031 CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1211 GGAAGAACGAACCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTT 1391 TAGCCATGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGTGTTCATCATT 1451 GTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTG 1620 1806 ATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCCCACAGTGCTTGATA 1865 840 780 901 CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 960 GGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTG 720 971 781 AAGGGGGTGTGATCCAAACTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAATATCTG TAATTAGTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAG AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTG 841 GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT TCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGT GGAAGAACGAACCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTT TGAGGCACTGGTGGAATAAAAACCTGTATATTTTACTTTGTTGCTGCGGTAGTCTTGCCGC GTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTG GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT 1621 TTTAGACGAGATCATACCGGTAAAGCAGGAATG 661

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547 ACGAGCCTCCGGCCCCGCCTCCCTCCTCCCCGGCCAGCGTGAGCCCCCCAGGCAGAGC 606
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                                                              Claim 11; Page 72-74; 120pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding a bone marrow secreted protein designated BMS112.
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24-SEP-1998;
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AAZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or stromal cells. The proteins can exhibit cytokine, cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells and to treat myeloid or lymphoid cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell canemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of farythroid progenitor cells, and to treat various can suppression, to support the growth and proliferation of megakarycoytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to support the growth and conjunction with platelet transfusions, to treat stem cell disorders conjunction with platelet transfusions, to treat stem cell disorders conjunction with platelet transfusions, to treat stem cell disorders conjunction with platelet transfusions, to treat stem cell disorders. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where the conferce cartilage and/or bone growth in circumstances where the conferce and cartilage and/or bone growth in circumstances where the conferce and cartilage and/or bone growth in circumstances where the conferce and cartilage and/or bone growth in circumstances where the conferce and cartilage and/or bone growth in circumstances where the conferce and cartilage and or prompty and platelet to the improved fixation of artificial joints
New isolated human polynucleotide and secreted proteins can induce
                                                              production of other cytokines in certain cell populations
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DB 3; Length 1610;

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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 Primers useful for synthesizing full length cDNA clones and
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                                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping;
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Pred. No. 0;
0; Mismatches 1; 1
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AAK94408 standard; cDNA; 1694
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Matches 1598; Conservative
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P-PSDB; AAM93484.
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                                                                  1535 GTTCATCATCATAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATATCTTT
                                                                                                                                   TICCTATCTGAGGCACTGGTGGAATAAAAACCTGTATATTTTACTTTGTTGCAGATAGT
              GATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGT
                                           1475 GATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGT
                                                                         GTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                  human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method; ss; gene.
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Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotide primers (830 cDNAs) useful for synthesizing length human cDNAs.
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02-MAY-2000; 2000JP-00183865.
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                                          TGGAGAGGAGCCCGCCGCCGCCGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCC
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                             TGGAGAGGAAGCCCGCCGGCCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCCTGCCGCCC
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Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition. Claim 1; Page 495; 593pp; English

Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;

GGCGCCTCTTCTTAGTTGATTTAGTTGATGTTTCTCTGAAGTTTGCAGTGTTGATGTGGG 1059 1330 TGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCAACTGCACCGGATAAAGGAACTCA 1271 1750 CCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCCGCCAGCCCCGGCTCCCG 1691 1690 CCGCGCCCCCCCCCCCGGCCGGCCCCAAGCGCAGGGGCTCCTCGGGCTCAGTGGATG 1631 669 1630 AGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCTGTGATACGCTCCTCTGCAGTTGTTG 1571 819 1510 TGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCC 1451 879 1450 TGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAAT 1391 939 666 636 CCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCCAGGGGCTCCTCGGGCTCAGTG---- 692 700 ACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCC 759 760 TGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCC CCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCCGCCAGCCCCGGCTCCCG 820 IGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAAT 940 TGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGAACTGCACGATAAAGGAACTCA 880 CAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGT Gaps 90; 70.6%; Score 1581; DB 4; Length 1758; 96.5%; Pred. No. 0; 0; Indels 0; Mismatches Best Local Similarity 96.5 Matches 1661; Conservative 577 637 1000 693 Query Match

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1299 1359 1899 1959 2079 1091 1031 1419 1659 2019 GCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCAT 2139 1270 GGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGG 1211 GCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGA 1719 CCAATATAAGTAAATATAGATTATATATGTATAGTGTTTCACAAAGCTTAGACCTTTACC 1839 971 911 851 791 731 671 551 491 431 371 311 254 134 TCCAAAGCACATAAGCTAGAAGAAGAATATTTCTAGGAGCACTACCATCTGTTTTCAAC GCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACAT TATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTTGGCTCTCATTT cacrerreagrerrecretrarrangaacescareageacadagaracarrareras GACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGAT TGAAGCGCAAAGCTGAATGAAAACGCCCCAAAATAATTAGTAGGAGTTCATCTTTAAAGGG 1030 TGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTCATCTTTAAAGGG AGTITCACAGATCGTTGTTAGATCTTTATTTTTAGCCCATGCACTGTTGTGAGGAAAATT TAAACCGTAATCATATCTTTTTCCTATCTGAGGCACTGGTGGAATAAAAACCTGTATAT 730 TITACITIGITGCACATAGICITIGCCCCATCITGCCAAGITGCAGAAGATGGTGGAGACTAG 670 AAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGAT CAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTTA CAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTATATTAATTG TCCAAAGCACATAAGCTAGAAGAAGAATATTTCTAGGAGCACTACCATCTGTTTTCAAC ATGAAATGCCACACACACATAGAACTC---CAACATCAATTTCATTGCACAGACTGACTGTA Accretcrrcacretcrrcarcarcarcarcarcarcarcarcarcaracacrecretaracacra TAAACCGTAATCATATCTTTTTCCTATCTGAGGCACTGGTGGAATAAAAAACCTGTATAT TTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAG AAAAAAAAAAAAAAAGCCCTTTTTCAGTTTTGTGCACTGTGTATGGTCCGTGTAGATTGAT GCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGA TTCCAGCCACCACAGAGTGCTTGATATTTCAGAGTCAGTGATTGGTTATACATGTGAGT GITAATITITGICACAGAATCIAIGGACIGAATCIAAIGCITCCAAAAAIGITGITIT 1060 1240 1300 1360 850 1480 1720 1840 1900 370 193 1150 1180 1090 910 1420 790 1540 1600 1660 1780 1960 2020 2080 1210 970 610 550 490 430 310 253 ઠે ઠે 셤 Š 셤 8 셤 ઠે 셤 8 g ò 셤 ò 셤 8 셤 ઠે 셤 8 셤 8 8 Š 셤 δ 셤 8 셤 ò 셤 Š 셤 8 8

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This invention describes novel mucleic acid molecules that are associated with apoptosis and encode a polypeptide and are derived from a normalised come library (embryonic or liver) or clone collections, and the extent of apoptosis measured by cell death detection assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay or the CPRG assay anticheumatic, anticherulash, anticheumatory, hepatotropic, anticheumatic, anticherulash, antichellammatory, hepatotropic, virucide, cerebroprotective and antialcoholic activity and can be used for therapy. The polymucleotides also related vectors, hosts (or their extracts), encoded polypeptide (or their receptors) and/or agents that characterize activity (including antisense sequences) are used for inhibit their activity (including antisense sequences) are used for treatment or prevention of tumours, autoimmune or degenerative diseases and viral infections, specifically leukaemia, carcinoma, sarcoma, with hepatitis or influenza viruses, Alzheimer's, Huntington's or Epatkinson's diseases, reperfusion injury, stroke and alcoholic liver diseases. Detection of the polynucleotides and derived polypeptides can apoptosis-associated protein described in the disclosure of the invention.
TGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAG 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids involved in apoptosis, useful for diagnosis and treatment of e.g. tumors and degenerative disease, also related proteins, antibodies and modulators.
                        133 TGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis, cell death, cytostatic, neuroprotective, immunosuppressive, antirhumatic; antiarthritic; dermatological; antiinflammatory; hepatotropic; virucide, nootropic; anticonvulsant; antiparkinsonian; vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour; autoimmune disease; degenerative disease; viral infection; leukaemia; carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes; lupus; hepatitis; influenza viruses; Alzheimer's disease; Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
                                                                                          2200 TATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAA 2240
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           T; 0 U; 0 Other;
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                                 Score 1577.4;
Pred. No. 0;
0; Mismatches
          Sequence 1599 BP; 354 A; 452 C; 422 G; 371
                                 Query Match
Best Local Similarity 99.7%;
Matches 1592; Conservative
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This invention relates to a novel method for modulating the expression of a target gene in a cell. Specifically, it refers to the introduction into a call of a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene, where the duplex region comprises a manmalian miRNA target region i.e. a non-coding microRNA (miRNA) that required manmalian miRNA at a post-transcriptional level. The present invention describes a method for controlling ontogenesis of a mammali, function of a mammalian cell, differentiation of a mammalian cell or viability of a mammalian cell in the post-transcriptional phase, which comprises of introducing a plasmid vector comprising a promoter and nucleic acid concerningly, it provides a cell therapy method for treating cancer, immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis, parkinson's disease, or Alzheimer's disease) or an inflammatory disease by introducing into the cell the miRNA, siRNA silencing precursor to the miRNA or the plasmid vector. As such, they can be developed into miRNA or the plasmid vector. As such, they can be developed into the miRNA or the plasmid vector. As such, they can be developed into contropic, neuroprotective and anti-inflammatory activities and hence can be used for immunotherapy. This polynucleotide sequence is a human target gene whose expression is modulated by miRNAs of the invention.
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WPI; 2004-653393/63.
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1233 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTCATCTT 1292

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Bone remodelling; osteoporosis; human; gene;
                                                                                                                   18-JAN-2000; 2000US-00484970.
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                            Human bone remodelling gene
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                                                                                 US6426186-B1
                                                                Homo sapiens
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                                                                                                                                                                                                          The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone remodelling genes of the invention
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A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful in an array for the diagnosis of bone remodeling and osteoporosis associated
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Best Local Similarity 99.3%;
Matches 1539; Conservative
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                                   TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC
                                                                                                              CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTCATCTT
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE polypeptides, and other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue typertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may be useful in treating of BACE activity and in particular agents that may be useful in treating of nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
                                                                                                                                                                                   Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury; stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoC; Nogo-associated disease; metastasis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human NogoC protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowley A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 62-64; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                  DNA encoding human NogoC protein.
                                    ABK90135 standard; DNA; 1798 BP.
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(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2001; 2001GB-00001312.
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                                                                         ABK90135;
RESULT 11
ABK90135
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symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polymucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present nucleic acid sequence encodes the human NogoC Sequence 1798 BP; 540 A; 314 C; 392 G; 552 T; 0 U; 0 Other; techniques. The protein of the

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CAGACTGACTGTAGTTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAA 2066
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                                                   AGATTTATACCATTGTGGTTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAAC
rradaccririaccrircagccaccccacagiccricararricagagicagicarridgir
                                                                                                                                                                                                                                                    ATCTGTTTTCAACATGAAATGCCACACACATAGAACTCCAACAACATCAATTTCATTGCA
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Gulukota K, Graham JR;
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                           Gaps
   6; Length 1798;
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                                                   GGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGT
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  Score 1488.8; DB 6
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66.5%;
99.1%;
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Matches 1540;
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The invention relates to 625 polymucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridse to them. Also included are a vector comprising the polymucleotide, a host cell cansiformed with the vector, the proteins encoded by the polymucleotides antibodies that bind to the proteins encoded by the polymucleotides of the proteins or the expression of the polymucleotide. The polymucleotides can be used as probes for the identification and isolation of full length can be used as probes for the identification and isolation of full length as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, tungal infections, autoimmune thyroiditis and cheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and disease, and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Asthmaer's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopolesis, for treating myeloid or light of the 625 cDNA lympholo cell deficiencies. The present sequence is one of the 625 cDNA human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders. Claim 1; Page 173; 339pp; English

Sequence 1514 BP; 455 A; 258 C; 313 G; 488 T; 0 U; 0 Other;

sequences encoding a secreted protein

1143 1323 1083 1203 1263 CTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATT 1023 843 180 963 240 300 360 420 480 540 783 GCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTA 120 903 541 GCCCAAAATAATTAGTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGG 600 9 CTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATT 1144 ATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAG GCCCAAAATAATTAGTAGGGGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGG 121 GGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGG 1 AGAAGACTGGAGTGTTTGGTGCCGGCCTATTCCTGCTGCTTTCATTGACAGTATTCA CATATICTGGAATICTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTICTG 181 CATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTG 1024 TAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGGTATTTACCTATGTTGGTGCCTTGT TTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTT 421 ATGAACGCCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAG 724 AGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCA GCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTGTGACCATCAGCTTTA GGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGG 301 TAGTIGATICTCTGAAGTITGCAGTGTGATGTGGGGTATTTACCTATGTTGGTGCCTTGT TTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTT Gaps Score 1473.4; DB 6; Length 1514; Pred. No. 2e-297; 0; Mismatches 6; Indels 7; Ouery Match 65.8%; Best Local Similarity 99.1%; Matches 1504; Conservative (241 1084 ' 361 964 784 904 61 844 셤 8 8 8 셤 ò g ઠે 유 ઠે 요 ઠે ò 셤 ò 셤 ઠે ò g

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AAD08386 standard; cDNA; 1683

(first entry)

09-AUG-2001

AAD08386;

RESULT 13 AAD08386 ID AAD0 XX AC AAD0 XX DT 09-A

1619 1739 1799 1080 1859 1140 1919 2039 2159 1497 1383 1443 1502 1679 1020 1200 1317 2099 1377 2219 1559 1378 TGCAAGAAATTATTAATTATAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGA 1437 900 720 840 960 2160 ACTABATCTGTGGBATGCATTGTGBACTGTBABAGCBABGTATCAATBABGCTTBTBGBC 1438 ACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTTATAGAC 601 AGGGTCAGGGAAGAACGAACCTTGACGTTGCAGGTTTCACAGATCGTTGTTAGATC 781 TATCTATCTGAGGCACTGGTGGAATAAAAAACCTGTATATTTTACTTTGTTGCTGCAGATAGT TTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAA TGTTCTAGGTGTATTGTGACTTTTTACTGTTATTATTTGCCAATATAAGTAAATATAGA TGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGA TTATATATATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCCCACAGTGC TTATATATATATATGTATACACAAAGCTTAGACCTTTACCTTCCAGCCACCCCACAGTGC TTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTGTAGTTCCAAAGCACATAAGCTAGA 1141 TIGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGA AGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAAATGCCACACATAG 1261 AACTC---CAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCACAGAATC TGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGA rrrarrrragecarecaererrereaseaaaarracererereaereererere 1444 ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTC-ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTTCC ---CTATCTGAGGCACTGGTGGAATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGT rrrrcagrirgiccacrereraregrecereracarrearecagarrircreaaareaaa AACTCCAACAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCACAGAATC 2220 TTAAAAAAAAAAAA 2236 1498 GTAAAAAACTTAGAAA 1514 1384 1560 1620 1680 1740 1800 1860 1920 1201 1980 2040 661 721 1503 901 1021 1081 961 2100 유 셤 셤 g 셤 q ò ð 셤 ઠે g ઠે ઠે ઠ 셤 ò à δ 셤 ð 셤 ò δ ð 유 ò 엄 Š

(HUMA-) HUMAN GENOME SCI INC

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Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; promised disorder; candoctrine disorder; promised disorder; celated disorder; c
protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52
                secreted
                                 Human
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sapiens Homo

secreted protein precursor" not include start codon" /partial 830..898 /*tag= b /*tag= c /*tag= c /*tag= c /product= "Mature human secreted protein" Location/Qualifiers 830. .1192 "Human does "CDS *tag≈ a 'product= 'note= sig_peptide mat_peptide Key

WO200077022-A1

21-DEC-2000

01-JUN-2000; 2000WO-US015136.

99US-0138629P 11-JUN-1999; Komatsoulis Rosen CA, Ruben SM,

3

WPI; 2001-367020/38. P-PSDB; AAE03939 Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.

Claim 1; Page 520; 614pp; English

The genes and their secreted proteins are useful for preventing, treating or amellorating medical conditions, e.g., by protein or gene therapy.

Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, cancer timeous, foetal and developmental abnormalities, disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, conversional disorders (e.g., Alzheimer's disease, Parkinson's disease), comitive disorders (e.g., Alzheimer's disease, parkinson's disease), comitive disorders, schizophrenia, asthma, skin disorders (e.g., angiogenic disorders, kidney disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proteins can also be used to aid wound healing and epithelial cell confidential and proteins can also be used to aid wound healing and epithelial cell confidential confidence transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. AAE03948-AAE03996 represent human secreted protein fragments or variants. partners, and in chemotaxis, and can be used as a food additive or

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preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the
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                                                                                                               Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
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                                                                                                                                                Score 1464.6; DB 4;
Pred. No. 1.4e-295;
1; Mismatches 0;
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Best Local Similarity 95.6%;
Matches 1544; Conservative
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94620-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately traingent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a) Polypeptides (ABP68596-ABF68637) encoded by (I) and oligomucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, r cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for inhibiting expression of the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
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                                                                                                                                                                              Hepler WT,
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
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                                                                                                                                                                              Lodes MJ,
21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631P.
12-UUL-2001; 2001US-0315999P.
27-NOV-2001; 2001US-0333626P.
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                                                                                                                                                                                                                  WPI; 2002-627435/67.
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cytostatic; tumour; gene; ss.
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31-JAN-2001; 2001US-0265682P.
09-FEB-2001; 2001US-0267568P.
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This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic cools for the management of, in particular, patients with systemic lupus erythematosis (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in order to achieve an improved diagnostic assay with sensitivity manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the diseases in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma, ankylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This polynucleotide is a DNA sequence representing human mRNA that is differentially expressed in patients with SLE, used in an exemplification
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                                                                                                                                                                                                              human; ds; autoimmune; chronic inflammatory disease; SLE;
systemic lupus erythematosis; rheumatoid arthritis; cholecystitis;
Sjogran; a disease; CREST syndrome; scleroderma; ankylosing spondylitis;
ulcerative colitis; primary sclerosing cholangitis; appendicitis;
diverticulitis; primary biliary sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one
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                                                                                                                                                                                 Human DNA differentially expressed in patients with SLE SegID96.
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96.1%; Pred. No. 8.2e-284;
ive 0; Mismatches 0;
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                                                                                   standard; DNA; 4632
                                                                                                                                                 (first entry)
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                                                                                                                                                  CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTCATCTT 3753
                                                                                                                                                                                 TTAATTGCCAATATAAGTAAATATAGATTATATATGTGTATGTGTTTCACAAAGCTTAGAC 4233
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August 1, 2005, 13:22:45 ; Search time 6519 Seconds (without alignments) 13079.301 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

9b est1: 9b est2: * * * * 9b est3: * * * * 9b est43: * * * 9b est6: * * 9b est6: * * 9b est6: * * 9b est6: * * * 9b est6: * * * 9b est6: * * 9b est6: * * 9b est6: * EST:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		ID Description	AF125103	AP077050 Homo Bapi	ZR611869 CR611869 full-leng	AK034902 Mus muscu	BX439214 BX439214	BX426504 BX426504 BX426504	BM469019 AGENCOURT		AL573494	BM450461 AGENCOURT	CK231727 ILLUMIGEN	BQ879359 A	CK232009 ILLUMIGEN	CN644030 CN644030 ILLUMIGEN	N647521 ILLUMIGEN	CO647477 CO647477 ILLUMIGEN	AL526343 AL526343 AL526343	CN644991	BQ959498 AGENCOURT		3X462171 . BX462171 BX462171	3M557554 AGENCOURT	CN803408 ILLUMIGEN	- 170-LI TIL COCAFFOO
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		Score	1488.8	1359.2	1355	1035.4	957.4	917.2	885	881.2	861.2	844.6	844.2	837.2	831.8	831	819.2	815.6	803.4	799.4	797.6	781.4	779.8	779.6	776.2	700
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ALIGNMENTS

AF125103 1798 bp mRNA linear HTC 22-MAY-2001 Homo sapiens neuroendocrine specific protein c homolog mRNA, AF125103 AF125103.1 G1:5107001 HTC.	Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases I to 1798) Zhang, Q. H., Ye, M., Wu, X. Y., Ren, S. X., Zhao, M., Zhao, C. J., Fu, G., Shen, Y., Fan, H. Y., Lu, G., Zhong, M., Xu, X. R., Han, Z. G., Zhang, J. W.,	Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells Genome Res. 10 (10), 1546-1560 (2000)	s 1 hang Huar hed	3 (Dases I to 1798) Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H., Dai, M., Huang, Q., Chen, S. and Chen, Z. Direct Submission Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China	11798; // Cogarism="Homo sapiens" // mol_type="mRNA": 1960e" // db xref="mRNA": 1960e" // cell type="CD34+ hematopoietic stem/progenitor cells" 215.
RESULT 1 AF125103 LOCUS DEFINITION ACCESSION VERSION SERVEDS SCHECE	ORGANISM REFERENCE AUTHORS	TITLE JOURNAL MEDIINE	MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	SOUTCE

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LGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLLQCSC YLERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"	Query Match 66.5%; Score 1488.8; DB 3; Length 1798; Best Local Similarity 99.1%; Pred. No. 0; Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;	ACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGT 	Oy 752 CCTATTCCTGCTGCTTTCATAGAGAGTATTCAGCATTGTGGGGGTAACAGCCTACATTGC 811 Db 307 CCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC 366	Oy 812 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT 871 Db 367 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCAAGCTAT 426	Oy 872 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 931	Oy 932 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGGTCATGTGAACTGCACGATAAA 991	Oy 992 GGAACTCAGGCGCCTCTTAGTTGATTAGTTGATTTCTCTGAAGTTTGCAGTGTT 1051 Db 547 GGAACTCAGGCGCCTCTTCTTAGTTGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT 606	QY 1052 GATGIGGGIATTTACTATGTTGCTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC 1111	Qy 1112 TCTCATTTCACT-CTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT	OY 1171 ATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAA 1230 	Qy 1231 TCCCTGGATTGAAGGGCAAAGTGAAAAGGCCCAAAATAATTAGTAGGAGTTCATC 1290 Db 786 TCCCTGGATTGAAGGGCAAAGTGAAAAGGCCCAAAATAATTAGTAGGAGTTCATC 845	Qy 1291 TTTAAAGGGGTATTCATTGTTATACGGGGGGGGGGTCAGGGAAGAACGAAC	Qy 1351 TIGCAGIGCAGITICACAGAICGTIGITAGAICTITIAIAGCCAIGCCAI	OY 1411 GGAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTAT 1470 Db 966 GGAAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTAT 1025	Qy 1471 GTATGGATTTAAACCGTAATCATTTTTCCTATCTGAGGCACTGGTGGAATAA 1526 Db 1026 GTATGGATTTAAACCGTAATCATATTTTCCTATCTGAGGCACTGGTGGAATAA 1085	OY 1527 AAAACCTGTATATTTACTTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAG 1586	Qy 1587 ATGGTGGAGCTAGAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTATGGTC 1646 Dh 1148 ATGGTGGAGCTAGAAAAAAAAAAAAAAAAAAAAAAAAAA	1647 CGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGGTTTAGACGAGATCATACCGGT

	RESULT 4 AK034902 AK034902 AK034902 AK034902 Mus musculus 12 days embryo embryonic body between diaphragm region and neck coDAR. RIKEN full.length enriched library. clone:9430059L06 product:RETICULON 4 (RUGHITE OUTGROWTH INHIBITOR) (WOGO PROTEIN) (FOOCEN) (CLUTY VESICLE 20 KDA PROTEIN) homolog [Rattus rocregicus], full insert sequence. AK034902.1 G1:26084268 AKC04902.2 G1:26084268 MUS musculus (Rouse mouse) MUS musculus (Rouse mouse) MUS musculus (Rouse mouse) MUS musculus (Rodentia; Sciurognathi; Muridae; Murinae; Mus anserius rocreated companies) AUTHORS (Carninci, P. and Hayashizaki, Y. Hayatsu, N., Sugahara, Y., Shibata, K., 1TILE MET. Enzymol. 303, 19-44 (1999) MUSDINUS BURBERORS AUTHORS (Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., 1TILE Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes companies. The selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes and managed to the selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes and managed to the selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes and managed to the selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes and managed to the selected CDNAs to selected Shibata K., Todawak. T. Tanaka, T. Matamas T. Tanaka, T. Matamas M. Mata	MEDLINE 20530913 PUBMED 11076861 REFERENCE 4
### \$60.5%; Score 1355; DB 3; Length 1540; ###################################	1111 1171 634 1231 694 1291 754 1351 1411 1471 934 1527 1054 11647	GTGTAGATTGATGATGTTTCTGAAATGTTTGTTTAGACGAGATCATACGGGTA 1707 MEI
Query Match 60.5%; Best Local Similarity 99.5%; Matches 1382; Conservative Qy 692 GGTTGTTGACCTCCTGTACT Qy 752 CCTATTCCTGCTGCTTTCA Qy 752 CCTATTCCTGCTGCTTTCA Qy 812 CTTGGCCTGCTGCTTTCA Qy 812 CTTGGCCTGCTCTTTCA Qy 872 CCTATTCCTGCTGCTTTCA Qy 872 CTATTCTGCTGCTTTCA Qy 872 CTGGAATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1052 515 1112 575 1172 635 1232 695 1352 815 1472 935 1528 1528 1528 1528 1528	Oy 1648 GTGTAGATTGATGCAGATT'

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TITLE FUNCTIONAL AUTHORS THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. TITLE FUNCTIONAL AUTHORS SECTIONAL SECTION OF a full-length mouse cDNA collection SEPERENCE SAUTHORS THE FANTOM CONSORTIUM and the RIKEN Genome Exploration Research Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Malysis of 60,770 full-length cDNAs (Adachi, J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Ruda, S., Furuno, M., Haramoto, K., Hiraoka, T., Hirozane, T., Hayatsu, M., Hayatsu, M., Hiraoka, T., Hiraoka, T., Koda, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Nowla, M., Nakamura, M., Mixana, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Sainagawa, A., Shiraki, T., Sakai, K., Sakai, K., Shinagawa, A., Takakaki, T., Takaki, Y., Saaki, Y., Tagami, M., Tagawa, A., Takabashi, F., Takaku, A., Takakashi, F., Takaku, A., Takabashi, F., Tagami, M., Takabashi, F., Tagami, M., Tagawa, A., Takabashi, F., Tagami, M., Tagawa, A., Takabashi, F., Tagami, M., Takabashi, F., Tagami,	Muramatsu, M. and Hayashizaki, Y. Direct Submission JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) COMMENT CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to		ORIGIN ORIGIN Query Match Qu

S-PRIME, mRNA sequence. WERSION BX439214.2 GI:47020895 KEYWORDS ST. SOURCE Home sapiens (human) BRATYCE; Home sapiens (human) BRATYCE; Home sapiens (human) BRATYCE; Home sapiens (human) BRATYCE; Home sapiens (human) MAMMALIA; Eutheria; Primates; Catarrhini; REFERENCE I, W.B., Gruber, C., Jessee, J. and Polayes, TITLE Full-length CDNA hibraries and normalizat: Unpublished (2001) COMMENT COMMENT On May 15, 2003 this sequence version rep; Contact: Genescope Co	Match
1276 FAGTAGGAGTICATCTTTAAAGGGGATATTCATTTATATCGGGGAGGGGA	1862 GATATTTCAGACTCACTCATTGCTTATACATGTTTCCAAAGCACATAACTAGAG 1921

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ucted by Life Technologies, a t strand cDNA was primed Five prime end enriched, d with Not I and cloned into he pCMVSPORT 6 vector. 1; GCGCCGCAGCAGCTGCAGCATC 120 AGRICCACCGCCCTGCCGCC 360 CCCCTCTCAGTCCTCCCCAACCC 60 CCTCTGGTCTCGTCCTCGGACA 180 421 CGGCCGCTCCCCCCGTCGCCCCCGGAGCGGCCGTCTTGGGACCCGAGCCCGGTGTCGT 480 CCTCTGGTCTCGTCCTCGGACA 254 GTGAGGGAGCCCGAGGACGAGG 240 GACCTGGAGGAGCTGGAGGTGC 300 CCGCCCCCGGGACCCCTGC 420 Vertebrata; Euteleostomi; ; Hominidae; Homo.); Length 1097;); Indels 1; Gaps r 1423.r see :008BD02QP1&c=1423.r. placed gi:30787776. es, D. ò

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/close lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned it the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                           organism="Homo sapiens"
                                                           /mol_type="mRNA"
/db xref="taxon:9606"
    ocation/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NoLI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
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BX426504 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
clone CSOBH001YJ01 3-PRIME, mRNA sequence.
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1 (Dases 1 to 1028)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Fill-length CDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30784554.
                                                                                                                                                                                                                                            CAGAGCCCGTGTGGSCCCCGCCASCCCCGGCDCCCGCSGSVCCCCCCTCCAMCCCGGGCG
                                                                                                                                                                                                                                                                                                                        GCCCCAAGCGCAGGGGSTCCTCGGGSTCAGKGGKTGTKGACCTCTGTACTGGAGAGACA
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                                                             CGACCGTGCCCGCCGATCCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTG
                                                                                                                                                                                                                       CAGAGCCCGTGTGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCG
division of Invitrogen.
This sequence balongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAH001CE01NP1&c=1423.r.
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AL549191 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
COLONE CSODIO51YB11 5-PRIME, mRNA sequence.
AL549191
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 911)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                 181 GGGGGGGTCAGGGAAGAACGAACCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTA
                                                                                                                                                                                              241 GAICTTTATTTTTAGCCATGCATGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Primates; Catarrhini; Hominidae; Homo.

S. 1 (bases 1 to 1003)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Longublished (1999)

Email: cgapbs-remail.nih.gov

Tissue Procurement: Arcc

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM12356 row: j column: 10

High quality sequence stop: 689.

Location/Qualifiers

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//organism=Homo sapiens"
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                                                                                   2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT 6445901 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587305 BM469019
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                                                                                                                                                                                           2095 IGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCAFTGTGGTTTAAAGCTGT 2154
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                                                                                                               182 GAATCTANGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTGCAAATATCAAACAT
                                                                                   GAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTTGCAAATATCAAACAT
                                                                                                                                                                                                                            122 TGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATATACCATTGTGGTTTAAAGCTGT
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On Feb 16, 2001 this sequence version replaced gi:31294840.

Contact: Genoscope denoscope.

Contact: Genoscope controlled Sequencage

Email: Sequence controlled Solory EVRY cedex - FRANCE

Email: Sequence cons.fr, Web: www.genoscope.cns.fr

1st strand coNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand coNA was digested with Not I and cloned
into the Not I and ECOR V sites of the pCWVSPORT 6 vector. Library
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AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI051YB11 3-PRIME, mRNA sequence.
AL573494.3 GI:46246666
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-errand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                           GCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCTGCTCTCTGTGACCATCAGCTTTA 843
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1. (bases 1 to 875)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDBA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGCGCA-GGGGCTCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTA
                                                                                                                                                                                                             AGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCA
                                                                                                                                                                                                                                           AGAAGACTGGAGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCA
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Pred. No. 8.6e-179;
2; Mismatches 10; Indels 0
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Best Local Similarity 98.6
Matches 863; Conservative
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                                                                                                                            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: sequetef@genoscope.cns.fr, Web : www.genoscope.cns.fr, Web : wew.genoscope.cns.fr, Web : sequence.cns.frv prime lst strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EOOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                      For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI051CA06QP1&c=1423.r. Location/Qualifiers
                           Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31271011.
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  and normalization
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; Pred. No. 3.4e-183;
14; Mismatches 8;
                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
Full-length cDNA libraries
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ilarity 97.5%;
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/mol type="mcMn"
//mol type="mcMn"
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/note="Gorgan: eys; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                    Data is capbs remail. nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bettp://image.llnl.gov
http://image.llnl.gov
Flate: LiAM12120 row: m column: 14
High quality sequence stop: 641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.7%; Score 844.6; DB 4; Length 1008; 96.7%; Pred. No. 4e-175; tive 0; Mismatches 25; Indels 7;
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/organism="Homo sapiens"
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Matches 926; Conservative
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AGENCOURT 6394193 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5494837
5', mRNA sequence.
BM450461
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
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CTATTCCTGCTGCTTTCATTRACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC
                                                                                                                                                     TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC
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RESULT 10 BM450461 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

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Query Match 37.7%; Score 844.2; DB 7; Length 1003; Best Local Similarity 95.6%; Pred. No. 4.9e-175; Matches 926; Conservative 0; Mismatches 28; Indels 15; Gaps · 5;	OY 858 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT 917	OY 918 GAAGTIGCTATATCTGAGGGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG 977	Oy 978 AACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTG 1037	OY 1038 AAGITIGCAGIGITGANGTGGGGTAITIACCTAIGTIGGIGCCTIGITIAAIGGICIGACA 1097 	OY 1098 CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAG 1157	Oy 1158 GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGTTATGGCTAAA 1217 	OY 1218 AICCAAGCAAAATCCCIGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATTA 1277 	OY 1278 GTAGGAGTICATCTTTAAAGGGGATATTCATTTGATTATGGGGGGGGGG	Qy 1338 ACGARCCTICACGIGCAGITGCAGITTCACAGATCGITGITAGATCITTATITITAGCCA 1397 Db 489 ACGAACCTICACATIGCAGITCAGAGATCGITGITAGATCITTATATITITAGCCA 548	QY 1398 TGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCATCATGTTAT 1457 DD 549 TGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCATCATCATATATAT	OY 1458 TGTAAGCTATGTATGATTTAAACGTAATCATATCTTTTCCTATCTGAGGCACTG 1517	Qy 1518 GTGGAATAAAAACCTGTATATTTTACTTTGTGCGATGTTTGCCGCATCTTGGCAA 1577	Qy 1578 GTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTG 1637	Qy 1638 IGHALTGECCGGGGTTGATGCCCGGATTTTCTGAAATGAATGTTTGATTTAGACGAGAT 1697 Db 780 IGHALGGTCCGTGTAGATTGATGATGAATTTTCTGAAATGAAA	Qy 1698 CATACCGGTAAAGCAGAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTG 1757	Qy 1758 ACTTTTACTGTTATATTAATTG-CCAATATAAGTAAA-TATAGATTATATATATATGTG 1815 	Qy 1816 TTTCACAAA 1824	Db 956 GTTTCCCAA 964
QY 1818 TCACAAAGCTTAGACCTTTACCTTCCACCACCACAGTGCTTGATATTCAGAGTCAG 1877	OY 1878 TCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAAAAATATTCTAGG 1937	OY 1938 AGCACTACCATCTGTTTTCAACATGAAATGCCACACATAGAACTTCCAACATCAAT 1997 	OY 1998 TTCATTGCACAGACTGACTGAGTTAATTTGTCACAGAATCTAGGACTGAATCTAATG 2057 	Qy 2058 CTTCCAAAATGTTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAA-T 2116 	OY 2117 TACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGG 2172	i c	ION ILLUMIGEN MCQ_2869 Katze MMBR Macaca mulatta cDNA 5' similar to human RTN4 (HB.436349), mRNA sequence.	VENSION CAST/2/.1 G1:39638085 KEYWORDS EN Acaca mulatta (rhegus monkey) ORGANISM Macaca mulatta		AUTHORS KAIZE, M.G., TOOMAB, M., KOYID, M., LACODACO, S.P., and Magness, C.L., TITLE Large-scale Rhesus Macaque cDNA Sequencing JOURNAL Unpublished (2003) COMMENT Contact: C. Magness	111Umlgen bloBclences inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408	Email: cmagness@illumigen.com Sequenced on 2003.11.24. 765 Q20 bases. Assembles in contig w/ 2 member(s). Contig contains 1 (1.5%) lib members. PCR PRimers	FORWARD: CCCTACTAAAGGAACAAA BACKWARD: CACTAIAGGGAATGGGTA Insert Length: 1003 Std Brzor: 0.00 Plate: CL000105 row: D column: 03		/organism="Macaca mulatta" /mol_type="mRNA" /strain="Indian" /db_xref="taxon:9544"	LR." R."	/note="Organ: brain; Vector: Uni-ZAP KR ; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP - $CDNA$ Synthesis kit (catalog #200400) and ZAP - $CDNA$ Gigaback III Gold	Cloning Kit (Catalog #200450)" ORIGIN

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ILLUMIGEN MCQ 3196 Katze MMPL2 Macaca mulatta cDNA 5' similar to human RTN4 (Hs.436349), mRNA sequence.
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                         TGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCAC 1161
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(Ecropithecinae, Macaca.

1 (Sassa 1 to 1164).

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rheeus Macaque CDNA Sequencing Unpublished (2003).

Contact: C. Magness

Illumigen Biosciences Inc.
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Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.11.25. 797 Q20 bases. Assembles in contig w/
member(s). Contig contains 1 (0%) lib members.
PCR PRIMETS
FORWARD: CCCTCACTAAAGGGAACAAAA
                                                AAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAAGCCCCAAAATAATTAGTAG
                                                                                                                                                                                                                                                                                                                   CTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTA
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Macaca mulatta
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/lab_host="Blide"
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/clone lib="Lupski dorsal root ganglion"
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Not!; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACGCGCCCCC-3' and adaptors:
5'-GACTAGTTCTAGATCGCGAGCGGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                  AGENCOURT 8119868 Lupski dorsal_root_ganglion Homo sapiens cDNA
Clone IMAGE:6177832 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 TIGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACT 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 TTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTAC 299
                                                                                                                                                                                                                                                            E (bases 1 to 901)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lln.gov
Plate: LiAM15556 row: g column: 17
High quality sequence stop: 609.
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                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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Matches 881; Conservative
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11. MAY-2004
ILLUMIGEN MCQ 9342 Katze MMBR Macaca mulatta cDNA clone IBIUW:8837
S' similar to Bases 1 to 955 highly similar to human RTN4
(H8.436449), mRNA sequence.
      1536 ATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGGATGGTGGAG 1595
                                                                                                                                                              TTGATGCAGATTTTCTGAAATGAATGTTTGTTTAGACGAGATCATA-CCGGTAAAGCAG 1713
                                                                                                                                                                                                                                            1714 GAATGACAAAGCTTGCTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATAT 1773
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                                                                                                      826 TTAG------AAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCCGTGTAGA 877
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/lab_host="R. coli SOLR"
/clome lib="Ka.coli SOLR"
/note="Corgan: braÎn; Vector: Uni-ZAP XR; Site_1: EcoR I;
Stq. 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis kit [catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                 878 TTGATGCAGATTTTCTGAAATGAAA----TGTTTAGACAAGATCATACCCAGTAAAGCAG 933
                                                                                                                                                                                                                                                                 934 GAATGAAAAATCTTGCTTTTCTGGTATGTTCTAGGGGTATTGGGGACTTTTACTGGTATAT 993
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Catarrhini; Cercopithecidae;
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Cercopithecinae, Macaca.

I (bases 1 to 956)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque CDNA Sequencing
Unpublished (2003)

Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 20637804008
                                                                                    CTAGAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGT-CCGTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cmagness@illumigen.com
Sequenced on 2004.01.21. 801 Q20 bases
PCR PRimers
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 956 Std Brror: 0.00
Plate: CL000070 row: A column: 10
Seg primer: CCCTCACTAAAGGGAACAAAA
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/organism="Macaca mulatta"
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                                                                                                                                                                                                                                                                                                                                                                                                       1832 CCTTTACCTTCCAGCCACCCCAC 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (rhesus monkey)
Macaca mulatta
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                                                                                                                                                                                                                                        /dev_stage="newborn infant"
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/clone lib="Kaze MMFLZ"
/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR
/note="Organ: placenta; Vector Strategene ZAP-cDNA
Synthes is the (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning Kit (Catalog #200450)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAAC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 GGATTGAAGCGGAAAGCTGAATGAAAACACCCAAAATAATTACTAGGAGTTCATCTTAA 526
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POLYANO.

    1164
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                                                                                                    Location/Qualifiers
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Best Local Similarity
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ILLUMIGEN MCQ 28658 Katze MMBR Macaca mulatta cDNA clone IBIUW:7529
5' similar to Bases 129 to 1018 highly similar to human RTN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone lib="Kaze MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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                                                                                                                                                                                            Cercopithecinae; Macaca.

1 (bases 1 to 1031)

Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rheeus Macaque CDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GETTGTTGACCTCCTCTACTGGAGAGACATGAAGAAGACTGGAGTGCTGTTTGGTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 CCAGADATCAGATGAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGAACTGCACGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 GGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 GGAACTCAGGGGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 36.6%; Score 819.2; DB 7; Length al Similarity 95.6%; Pred. No. 1.6e-169; 864; Conservative 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                         Fax: 2063780408
Email: cmagness@illumigen.com
Seguenced on 2004.03.24. 773 Q20 bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGGGAATTGGGTA
Insert Lengch: 1031 Std Brror: 0.00
Plate: CL000187 row: G column: 05
Seg primer: CCCTCACTAAAGGGAACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1031
/organism="Macaca mulatta"
/mol type="mRNA"
/strain="Indian"
/db xref="taxon:9544"
/clone="IBIUW:7529"
                                                                                                                     Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                    (Hs.436349), mRNA sequence
                                                          CN647521
CN647521.1 GI:47160964
                                                                                                                                         Macaca mulatta
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Best Local S:
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                       1 GAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATCTGAGGAGTTGGTT
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                                                            15;
                        Length 956;
                                                          30; Indels
                      Score 831; DB 7;
Pred. No. 4e-172;
0; Mismatches 30
                      Query Match
Best Local Similarity 95.3%;
Matches 914; Conservative
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788 TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTACCCATGCCCTGTTGTGAG 847
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                                                                                          GATGTGGGTATTTACCTATGTTGCCTTCTTTAATGGTCTGACACTACTGATTTTGGC 1111
                                             1172 TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT 1231
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